TITLE OF THE INVENTION

CONE SNAIL PEPTIDES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is related to and claims priority under 35 USC §119(e) to U.S. provisional patent application Serial No. 60/267,408 filed 9 February 2001, incorporated herein by reference.

[0002] This invention was made with Government support under Grant No. PO1 GM48677 awarded by the National Institute of General Medical Sciences, National Institutes of Health, Bethesda, Maryland. The United States Government has certain rights in the invention.

BACKGROUND OF THE INVENTION

[0003] The present invention is directed to conotoxin peptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated ion channels, ligand-gated ion channels and/or receptors. The invention is further directed to nucleic acid sequences encoding the conotoxin peptides and encoding propeptides, as well as the propeptides.

[0004] The publications and other materials used herein to illuminate the background of the invention, and in particular, cases to provide additional details respecting the practice, are incorporated by reference, and for convenience are referenced in the following text by author and date and are listed alphabetically by author in the appended bibliography.

[0005] *Conus* is a genus of predatory marine gastropods (snails) which envenomate their prey. Venomous cone snails use a highly developed projectile apparatus to deliver their cocktail of toxic conotoxins into their prey. In fish-eating species such as *Conus magus* the cone detects the presence of the fish using chemosensors in its siphon and when close enough extends its proboscis and fires a hollow harpoon-like tooth containing venom into the fish. This immobilizes the fish and enables the cone snail to wind it into its mouth via an attached filament. For general information on *Conus* and their venom see the website address http://grimwade.biochem.unimelb.edu.au/cone/referenc.html. Prey capture is accomplished through a sophisticated arsenal of peptides which target specific ion channel and receptor subtypes. Each *Conus* species venom appears to contain a unique set of 50-200 peptides. The

composition of the venom differs greatly between species and between individual snails within each species, each optimally evolved to paralyse it's prey. The active components of the venom are small peptides toxins, typically 12-30 amino acid residues in length and are typically highly constrained peptides due to their high density of disulphide bonds.

[0006] The venoms consist of a large number of different peptide components that when separated exhibit a range of biological activities: when injected into mice they elicit a range of physiological responses from shaking to depression. The paralytic components of the venom that have been the focus of recent investigation are the α-, ω- and μ-conotoxins. All of these conotoxins act by preventing neuronal communication, but each targets a different aspect of the process to achieve this. The α-conotoxins target nicotinic ligand gated channels, the μ-conotoxins target the voltage-gated sodium channels and the ω-conotoxins target the voltage-gated calcium channels (Olivera et al., 1985; Olivera et al., 1990). For example a linkage has been established between α-, αA- & ϕ-conotoxins and the nicotinic ligand-gated ion channel; ω-conotoxins and the voltage-gated calcium channel; μ-conotoxins and the voltage-gated sodium channel; δ-conotoxins and the voltage-gated sodium channel; κ-conotoxins and the voltage-gated potassium channel; conantokins and the ligand-gated glutamate (NMDA) channel.

[0007] However, the structure and function of only a small minority of these peptides have been determined to date. For peptides where function has been determined, three classes of targets have been elucidated: voltage-gated ion channels; ligand-gated ion channels, and G-protein-linked receptors.

[0008] *Conus* peptides which target voltage-gated ion channels include those that delay the inactivation of sodium channels, as well as blockers specific for sodium channels, calcium channels and potassium channels. Peptides that target ligand-gated ion channels include antagonists of NMDA and serotonin receptors, as well as competitive and noncompetitive nicotinic receptor antagonists. Peptides which act on G-protein receptors include neurotensin and vasopressin receptor agonists. The unprecedented pharmaceutical selectivity of conotoxins is at least in part defined by a specific disulfide bond frameworks combined with hypervariable amino acids within disulfide loops (for a review see McIntosh et al., 1998).

[0009] There are drugs used in the treatment of pain, which are known in the literature and to the skilled artisan. See, for example, Merck Manual, 16th Ed. (1992). However, there is a demand for more active analgesic agents with diminished side effects and toxicity and which are non-addictive. The ideal analgesic would reduce the awareness of pain, produce analgesia over a

wide range of pain types, act satisfactorily whether given orally or parenterally, produce minimal or no side effects, be free from tendency to produce tolerance and drug dependence.

[0010] Due to the high potency and exquisite selectivity of the conopeptides, several are in various stages of clinical development for treatment of human disorders. For example, two *Conus* peptides are being developed for the treatment of pain. The most advanced is ω-conotoxin MVIIA (ziconotide), an N-type calcium channel blocker (see Heading, C., 1999; U.S. Patent No. 5,859,186). ω-Conotoxin MVIIA, isolated from *Conus magus*, is approximately 1000 times more potent than morphine, yet does not produce the tolerance or addictive properties of opiates. ω-Conotoxin MVIIA has completed Phase III (final stages) of human clinical trials and has been approved as a therapeutic agent. ω-Conotoxin MVIIA is introduced into human patients by means of an implantable, programmable pump with a catheter threaded into the intrathecal space. Preclinical testing for use in post-surgical pain is being carried out on another *Conus* peptide, contulakin-G, isolated from *Conus geographus* (Craig et al. 1999). Contulakin-G is a 16 amino acid O-linked glycopeptide whose C-terminus resembles neurotensin. It is an agonist of neurotensin receptors, but appears significantly more potent than neurotensin in inhibiting pain in *in vivo* assays.

[0011] In view of a large number of biologically active substances in *Conus* species it is desirable to further characterize them and to identify peptides capable of treating disorders voltage-gated ion channels, ligand-gated ion channels and/or receptors. Surprisingly, and in accordance with this invention, Applicants have discovered novel conotoxins that can be useful for the treatment of disorders involving voltage-gated ion channels, ligand-gated ion channels and/or receptors and could address a long felt need for a safe and effective treatment.

SUMMARY OF THE INVENTION

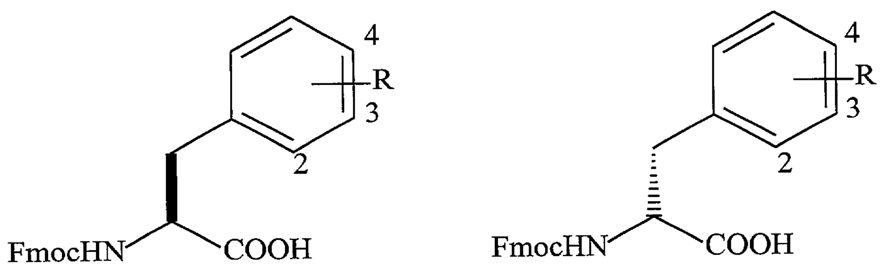
[0012] The present invention is directed to conotoxin peptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated ion channels, ligand-gated ion channels and/or receptors. The invention is further directed to nucleic acid sequences encoding the conotoxin peptides and encoding propeptides, as well as the propeptides.

[0013] More specifically, the present invention is directed to conotoxin peptides, having the amino acid sequences set forth in Tables 1-14 below.

[0014] The present invention is also directed to derivatives or pharmaceutically acceptable salts of the conotoxin peptides or the derivatives. Examples of derivatives include peptides in which the Arg residues may be substituted by Lys, ornithine, homoargine, nor-Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any synthetic basic amino acid; the Lys residues may be substituted by Arg, ornithine, homoargine, nor-Lys, or any synthetic basic amino acid; the Tyr residues may be substituted with meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any synthetic hydroxy containing amino acid; the Ser residues may be substituted with Thr or any synthetic hydroxylated amino acid; the Thr residues may be substituted with Ser or any synthetic hydroxylated amino acid; the Phe residues may be substituted with any synthetic aromatic amino acid; the Trp residues may be substituted with Trp (D), neo-Trp, halo-Trp (D or L) or any aromatic synthetic amino acid; and the Asn, Ser, Thr or Hyp residues may be glycosylated. The halogen may be iodo, chloro, fluoro or bromo; preferably iodo for halogen substituted-Tyr and bromo for halogen-substituted Trp. The Tyr residues may also be substituted with the 3-hydroxyl or 2-hydroxyl isomers (meta-Tyr or ortho-Tyr, respectively) and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic amino acid, e.g., tetrazolyl derivatives of Gly and Ala. The aliphatic amino acids may be substituted by synthetic derivatives bearing non-natural aliphatic branched or linear side chains C_nH_{2n+2} up to and including n=8. The Leu residues may be substituted with Leu (D). The Glu residues may be substituted with Gla. The Gla residues may be substituted with Glu. The N-terminal Gln residues may be substituted with pyroGlu. The Met residues may be substituted with norleucine (Nle). The Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L).

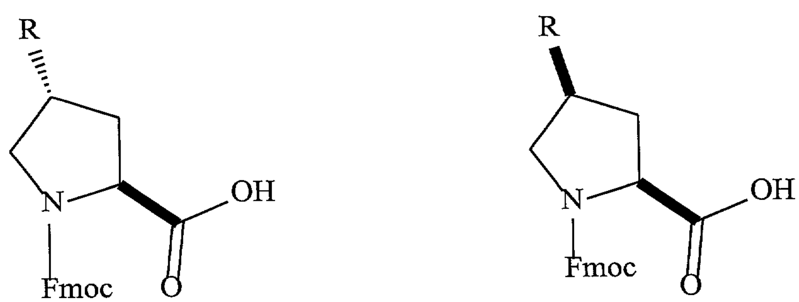
[0015] Examples of synthetic aromatic amino acid include, but are not limited to, nitro-Phe, 4-substituted-Phe wherein the substituent is C_1-C_3 alkyl, carboxyl, hyrdroxymethyl, sulphomethyl, halo, phenyl, -CHO, -CN, -SO_3H and -NHAc. Examples of synthetic hydroxy containing amino acid, include, but are not limited to, such as 4-hydroxymethyl-Phe, 4-hydroxyphenyl-Gly, 2,6-dimethyl-Tyr and 5-amino-Tyr. Examples of synthetic basic amino acids include, but are not limited to, N-1-(2-pyrazolinyl)-Arg, 2-(4-piperinyl)-Gly, 2-(4-piperinyl)-Ala, 2-[3-(2S)pyrrolininyl)]-Gly and 2-[3-(2S)pyrrolininyl)]-Ala. These and other synthetic basic amino acids, synthetic hydroxy containing amino acids or synthetic aromatic amino acids are described in Building Block Index, Version 3.0 (1999 Catalog, pages 4-47 for

hydroxy containing amino acids and aromatic amino acids and pages 66-87 for basic amino acids; see also http://www.amino-acids.com), incorporated herein by reference, by and available from RSP Amino Acid Analogues, Inc., Worcester, MA. The residues containing protecting groups are deprotected using conventional techniques. Examples of synthetic acid amino acids include those derivatives bearing acidic functionality, including carboxyl, phosphate, sulfonate and synthetic tetrazolyl derivatives such as described by Ornstein et al. (1993) and in U.S. Patent No. 5,331,001, each incorporated herein by reference, and such as shown in the following schemes 1-3.



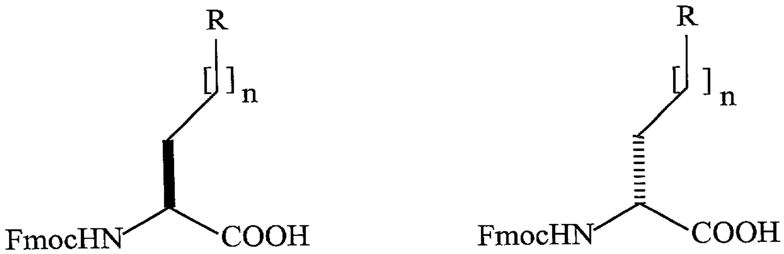
R=COOH, tetazole, CH_2COOH, 4-$NHSO_2CH_3$, 4-$NHSO_2$Phenyl, 4-CH_2SO_3H, SO_3H, 4-$CH_2PO_3H_2$, CH_2CH_2COOH, OCH_2Tetrazole, CH_2STetrazole, HNTetrazole, $CONHSO_2R_1$ where R_1 is CH_3 or Phenyl SO_2-Tetrazole, $CH_2CH_2SO_3H$, 1,2,4-tetrazole, 3-isoxazolone, amidotetrazole, $CH_2CH_2PO_3H_2$

Scheme 1



R = COOH, tetrazole, CH_2COOH, CH_2tetrazole

Scheme 2



R = COOH, tetazole, CH_2COOH, 4-$NHSO_2CH_3$, 4-$NHSO_2$Phenyl, 4-CH_2SO_3H, SO_3H, 4-$CH_2PO_3H_2$, CH_2CH_2COOH, OCH_2Tetrazole, CH_2STetrazole, HNTetrazole, $CONHSO_2R_1$ where R_1 is CH_3 or Phenyl SO_2-Tetrazole, $CH_2CH_2SO_3H$, 1,2,4-tetrazole, 3-isoxazolone, amidotetrazole, $CH_2CH_2PO_3H_2$; n = 0, 1, 2, or 3

Scheme 3

[0016] Optionally, in the conotoxin peptides of the present invention, the Asn residues may be modified to contain an N-glycan and the Ser, Thr and Hyp residues may be modified to contain an O-glycan (e.g., g-N, g-S, g-T and g-Hyp). In accordance with the present invention, a glycan shall mean any N-, S- or O-linked mono-, di-, tri-, poly- or oligosaccharide that can be attached to any hydroxy, amino or thiol group of natural or modified amino acids by synthetic or enzymatic methodologies known in the art. The monosaccharides making up the glycan can include D-allose, D-altrose, D-glucose, D-mannose, D-gulose, D-idose, D-galactose, D-talose, D-galactosamine, D-glucosamine, D-N-acetyl-glucosamine (GlcNAc), D-N-acetyl-galactosamine (GalNAc), D-fucose or D-arabinose. These saccharides may be structurally modified, e.g., with one or more O-sulfate, O-phosphate, O-acetyl or acidic groups, such as sialic acid, including combinations thereof. The gylcan may also include similar polyhydroxy groups, such as D-penicillamine 2,5 and halogenated derivatives thereof or polypropylene glycol derivatives. The glycosidic linkage is beta and 1-4 or 1-3, preferably 1-3. The linkage between the glycan and the amino acid may be alpha or beta, preferably alpha and is 1-.

[0017] Core O-glycans have been described by Van de Steen et al. (1998), incorporated herein by reference. Mucin type O-linked oligosaccharides are attached to Ser or Thr (or other hydroxylated residues of the present peptides) by a GalNAc residue. The monosaccharide building blocks and the linkage attached to this first GalNAc residue define the "core glycans," of which eight have been identified. The type of glycosidic linkage (orientation and

connectivities) are defined for each core glycan. Suitable glycans and glycan analogs are described further in U.S. Serial No. 09/420,797 filed 19 October 1999 and in PCT Application No. PCT/US99/24380 filed 19 October 1999 (PCT Published Application No. WO 00/23092), each incorporated herein by reference. A preferred glycan is Gal(β1→3)GalNAc(α1→).

[0018] Optionally, in the conotoxin peptides described above, pairs of Cys residues may be replaced pairwise with isoteric lactam or ester-thioether replacements, such as Ser/(Glu or Asp), Lys/(Glu or Asp), Cys/(Glu or Asp) or Cys/Ala combinations. Sequential coupling by known methods (Barnay et al., 2000; Hruby et al., 1994; Bitan et al., 1997) allows replacement of native Cys bridges with lactam bridges. Thioether analogs may be readily synthesized using halo-Ala residues commercially available from RSP Amino Acid Analogues. In addition, individual Cys residues may be replaced with homoCys, seleno-Cys or penicillamine, so that disulfide bridges may be formed between Cys-homoCys or Cys-penicillamine, or homoCys-penicllamine and the like.

[0019] The present invention is further directed to derivatives of the above peptides and peptide derivatives which are acylic permutations in which the cyclic permutants retain the native bridging pattern of native toxin. See, Craik et al. (2001).

[0020] The present invention is further directed to a method of treating disorders associated with voltage-gated ion channels, ligand-gated ion channels and/or receptor disorders in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a conotoxin peptide described herein or a pharmaceutically acceptable salt or solvate thereof. The present invention is also directed to a pharmaceutical composition comprising a therapeutically effective amount of a conotoxin peptide described herein or a pharmaceutically acceptable salt or solvate thereof and a pharmaceutically acceptable carrier.

[0021] More specifically, the present invention is also directed to nucleic acids which encode conotoxin peptides of the present invention or which encodes precursor peptides for these conotoxin peptides, as well as the precursor peptide. The nucleic acid sequences encoding the precursor peptides of other conotoxin peptides of the present invention are set forth in Table 1. Table 1 also sets forth the amino acid sequences of these precursor peptides.

[0022] Another embodiment of the invention contemplates a method of identifying compounds that mimic the therapeutic activity of the instant peptide, comprising the steps of: (a) conducting a biological assay on a test compound to determine the therapeutic activity; and (b)

comparing the results obtained from the biological assay of the test compound to the results obtained from the biological assay of the peptide. The peptide is labeled with any conventional label, preferably a radioiodine on an available Tyr. Thus, the invention is also directed to radioiodinated conotoxins.

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DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

[0023] The present invention is directed to conotoxin peptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated ion channels, ligand-gated ion channels and/or receptors. The invention is further directed to nucleic acid sequences encoding the conotoxin peptides and encoding propeptides, as well as the propeptides.

[0024] The present invention, in another aspect, relates to a pharmaceutical composition comprising an effective amount of a conotoxin peptides, a mutein thereof, an analog thereof, an active fragment thereof or pharmaceutically acceptable salts or solvates. Such a pharmaceutical composition has the capability of acting at voltage-gated ion channels, ligand-gated ion channels and/or receptors, and are thus useful for treating a disorder or disease of a living animal body, including a human, which disorder or disease is responsive to the partial or complete blockade of such channels or receptors comprising the step of administering to such a living animal body, including a human, in need thereof a therapeutically effective amount of a pharmaceutical composition of the present invention.

[0025] Examples of voltage-gated ion channels include the voltage-gated calcium channel, the voltage-gated sodium channel, the voltage-gated potassium channel and the proton-gated ion channel. Examples of ligand-gated channels include the nicotinic ligand-gated ion channel, ligand-gated glutamate (NMDA) channel and the ligand-gated $5HT_3$ (serotonin) channel. Examples of receptors include the G-protein receptors. Activity of ψ-conotoxins is described in U.S. Patent No. 5,969,096 and in Shon et al. (1997). Activity of bromosleeper conotoxins is described in U.S. Patent No. 5,889,147 and in Craig et al. (1997). Activity of σ-conotoxins is described in U.S. Patent No. 5,889,147. Activity of contryphan conotoxins is described in U.S. Patent No. 6,077,934 and in Jimenez et al. (1996). Activity of conopressins is described in Cruz et al. (1987) and in Kruszynski et al. (1990). Activity of γ-conotoxins is described in Fainzilber et al. (1998). Activity of αA-conotoxins (kappaA??) is described in

Jacobsen et al. (1997) and in Hopkins et al. (1995). Activity of α-conotoxins is described in U.S. Patent Nos. 4,447,356 and 5,514,774. Activity of τ-conotoxins is described in U.S. Serial No. 09/497,491 (PCT/US00/03021, PCT published application WO 00/46371) as an antagonist for acetylcholine receptors and as analgesic agents for the treatment of pain (whether acute or chronic), including migraine, chronic pain, and neuropathic pain, without undesirable side effects. Activity of contulakins is described in U.S. Serial No. 09/420,797 (PCT/US99/24380, PCT published application WO 00/23092). Each of these references is incorporated herein by reference.

[0026] Since σ-conotoxins are antagonists of the $5HT_3$ receptor, they are also useful in treating irritable bowel syndrome (IBS) and visceral pain. Visceral pain is a common experience in health and disease. Chronic visceral hyperalgesia in the absence of detectable organic disease has been implicated in many common functional bowel disorders (FDB), such as IBS, non-ulcer dyspepsia (NUD) and non-cardiac chest pain (NCCP).

[0027] Pain in IBS cannot be explained by normal perception of abnormal motility. In the majority of patients, sensory perception itself is abnormal. Most visceral afferent information is part of the reflex activity of digestion and does not reach concious perception. Increasing evidence suggests that long term changes in the the thresholds and gain of the visceral afferent pathways are present in patients with FDBs. This has been referred to as visceral hyperalgesia (Mayer et al., 1994).

[0028] It has been proposed that FDBs are a result of increased excitability of spinal neurones. According to their model, many inputs can result in transient, short term, or life long sensitization of afferent pathways involved in visceral reflexes and sensations from the gut. The increased sensory input to interneurons and / or dorsal horn neurons in the spinal cord will result in secondary hyperalgesia, in which adjacent, undamaged viscera develop sensitivity to normal innocuous stimuli (allodynia), and central hyperexcitability as a consequence of changes in the circuitary of the dorsal horn. This central sensitization may subsequently extend to supraspinal centers also.

[0029] Altered spinal processing of visceral sensory information can explain altered sensory thresholds and altered referral patterns, the perception of visceral sensations without stimulation of visceral mechnoreceptors (sensation of incomplete evacuation), and the symptomatic involvement of multiple sites in the GI tract, including extra intestinal sites. Increased excitability of dorsal horn neurones, resulting in the recruitment of previously sub-

threshold inputs, may explain cutaneous allodynia in some patients with IBS, burning sensations referred to different parts of the body, cold hypersensitivity and pain referral to upper and lower extremities.

[0030] A number of compounds have been shown to modulate visceral sensitivity in IBS patients. These include octreotide (sst_2; Novartis), the 5-HT_3 antgonists odansetron (Glaxo) and granisetron (SKB) and the peripheral kappa opioid agonist, fedotozine (Jouveinal SA). The 5-HT_3 antagonist alosteron (Glaxo), cuurrently in development for IBS, is active in modifying the perception of colonic distension and gut compliance in IBS patients. New drugs in development for the treatment of IBS that are targeted at pain control as well as dysmotility include 5-HT_3 and 5-HT_4 receptor antagonists. 5-HT_3 receptors are located throughout the central and peripheral nervous system – their role in modulating the activity of visceral afferent and enteric neurones has led to the proposal that 5-HT acts as a sensitizing agent via these receptors on visceral afferent neurones. 5-HT_3 receptor antagonists have been widely reported to attenuate blood pressure responses to intestinal distension. 5-HT_3 antagonists in development for IBS include Alosteron (phase III), which is reported to reduce abdominal pain, slow colonic transit and increase colon compliance in IBS patients. Other compounds with positive effects include the antiemetic Ramosteron (Yamanouchi), Cilansteron (Solvay) and YM-114 (Yamanouchi). An animal model for dysmotility of the GI tract has been described by Maric et al. (1989).

[0031] The conotoxin peptides described herein are sufficiently small to be chemically synthesized. General chemical syntheses for preparing the foregoing conotoxin peptides are described hereinafter. Various ones of the conotoxin peptides can also be obtained by isolation and purification from specific *Conus* species using the technique described in U.S. Patent Nos. 4,447,356 (Olivera et al., 1984); 5,514,774; 5,719,264; and 5,591,821, as well as in PCT published application WO 98/03189, the disclosures of which are incorporated herein by reference.

[0032] Although the conotoxin peptides of the present invention can be obtained by purification from cone snails, because the amounts of conotoxin peptides obtainable from individual snails are very small, the desired substantially pure conotoxin peptides are best practically obtained in commercially valuable amounts by chemical synthesis using solid-phase strategy. For example, the yield from a single cone snail may be about 10 micrograms or less of conotoxin peptides peptide. By "substantially pure" is meant that the peptide is present in the substantial absence of other biological molecules of the same type; it is preferably present in an

amount of at least about 85% purity and preferably at least about 95% purity. Chemical synthesis of biologically active conotoxin peptides peptides depends of course upon correct determination of the amino acid sequence.

[0033] The conotoxin peptides can also be produced by recombinant DNA techniques well known in the art. Such techniques are described by Sambrook et al. (1989). A gene of interest (i.e., a gene that encodes a suitable conotoxin peptides) can be inserted into a cloning site of a suitable expression vector by using standard techniques. These techniques are well known to those skilled in the art. The expression vector containing the gene of interest may then be used to transfect the desired cell line. Standard transfection techniques such as calcium phosphate co-precipitation, DEAE-dextran transfection or electroporation may be utilized. A wide variety of host/expression vector combinations may be used to express a gene encoding a conotoxin peptide of interest. Such combinations are well known to a skilled artisan. The peptides produced in this manner are isolated, reduced if necessary, and oxidized to form the correct disulfide bonds.

[0034] One method of forming disulfide bonds in the conotoxin peptides of the present invention is the air oxidation of the linear peptides for prolonged periods under cold room temperatures or at room temperature. This procedure results in the creation of a substantial amount of the bioactive, disulfide-linked peptides. The oxidized peptides are fractionated using reverse-phase high performance liquid chromatography (HPLC) or the like, to separate peptides having different linked configurations. Thereafter, either by comparing these fractions with the elution of the native material or by using a simple assay, the particular fraction having the correct linkage for maximum biological potency is easily determined. However, because of the dilution resulting from the presence of other fractions of less biopotency, a somewhat higher dosage may be required.

[0035] The peptides are synthesized by a suitable method, such as by exclusively solid-phase techniques, by partial solid-phase techniques, by fragment condensation or by classical solution couplings.

[0036] In conventional solution phase peptide synthesis, the peptide chain can be prepared by a series of coupling reactions in which constituent amino acids are added to the growing peptide chain in the desired sequence. Use of various coupling reagents, e.g., dicyclohexylcarbodiimide or diisopropylcarbonyldimidazole, various active esters, e.g., esters of N-hydroxyphthalimide or N-hydroxy-succinimide, and the various cleavage reagents, to carry

out reaction in solution, with subsequent isolation and purification of intermediates, is well known classical peptide methodology. Classical solution synthesis is described in detail in the treatise, "Methoden der Organischen Chemie (Houben-Weyl): Synthese von Peptiden," (1974). Techniques of exclusively solid-phase synthesis are set forth in the textbook, "Solid-Phase Peptide Synthesis," (Stewart and Young, 1969), and are exemplified by the disclosure of U.S. Patent 4,105,603 (Vale et al., 1978). The fragment condensation method of synthesis is exemplified in U.S. Patent 3,972,859 (1976). Other available syntheses are exemplified by U.S. Patents No. 3,842,067 (1974) and 3,862,925 (1975). The synthesis of peptides containing γ-carboxyglutamic acid residues is exemplified by Rivier et al. (1987), Nishiuchi et al. (1993) and Zhou et al. (1996).

[0037] Common to such chemical syntheses is the protection of the labile side chain groups of the various amino acid moieties with suitable protecting groups which will prevent a chemical reaction from occurring at that site until the group is ultimately removed. Usually also common is the protection of an α-amino group on an amino acid or a fragment while that entity reacts at the carboxyl group, followed by the selective removal of the α-amino protecting group to allow subsequent reaction to take place at that location. Accordingly, it is common that, as a step in such a synthesis, an intermediate compound is produced which includes each of the amino acid residues located in its desired sequence in the peptide chain with appropriate side-chain protecting groups linked to various ones of the residues having labile side chains.

[0038] As far as the selection of a side chain amino protecting group is concerned, generally one is chosen which is not removed during deprotection of the α-amino groups during the synthesis. However, for some amino acids, e.g., His, protection is not generally necessary. In selecting a particular side chain protecting group to be used in the synthesis of the peptides, the following general rules are followed: (a) the protecting group preferably retains its protecting properties and is not split off under coupling conditions, (b) the protecting group should be stable under the reaction conditions selected for removing the α-amino protecting group at each step of the synthesis, and (c) the side chain protecting group must be removable, upon the completion of the synthesis containing the desired amino acid sequence, under reaction conditions that will not undesirably alter the peptide chain.

[0039] It should be possible to prepare many, or even all, of these peptides using recombinant DNA technology. However, when peptides are not so prepared, they are preferably prepared using the Merrifield solid-phase synthesis, although other equivalent chemical

syntheses known in the art can also be used as previously mentioned. Solid-phase synthesis is commenced from the C-terminus of the peptide by coupling a protected α-amino acid to a suitable resin. Such a starting material can be prepared by attaching an α-amino-protected amino acid by an ester linkage to a chloromethylated resin or a hydroxymethyl resin, or by an amide bond to a benzhydrylamine (BHA) resin or paramethylbenzhydrylamine (MBHA) resin. Preparation of the hydroxymethyl resin is described by Bodansky et al. (1966). Chloromethylated resins are commercially available from Bio Rad Laboratories (Richmond, CA) and from Lab. Systems, Inc. The preparation of such a resin is described by Stewart and Young (1969). BHA and MBHA resin supports are commercially available, and are generally used when the desired polypeptide being synthesized has an unsubstituted amide at the C-terminus. Thus, solid resin supports may be any of those known in the art, such as one having the formulae -O-CH_2-resin support, -NH BHA resin support, or -NH-MBHA resin support. When the unsubstituted amide is desired, use of a BHA or MBHA resin is preferred, because cleavage directly gives the amide. In case the N-methyl amide is desired, it can be generated from an N-methyl BHA resin. Should other substituted amides be desired, the teaching of U.S. Patent No. 4,569,967 (Kornreich et al., 1986) can be used, or should still other groups than the free acid be desired at the C-terminus, it may be preferable to synthesize the peptide using classical methods as set forth in the Houben-Weyl text (1974).

[0040] The C-terminal amino acid, protected by Boc or Fmoc and by a side-chain protecting group, if appropriate, can be first coupled to a chloromethylated resin according to the procedure set forth in K. Horiki et al. (1978), using KF in DMF at about 60°C for 24 hours with stirring, when a peptide having free acid at the C-terminus is to be synthesized. Following the coupling of the BOC-protected amino acid to the resin support, the α-amino protecting group is removed, as by using trifluoroacetic acid (TFA) in methylene chloride or TFA alone. The deprotection is carried out at a temperature between about 0°C and room temperature. Other standard cleaving reagents, such as HCl in dioxane, and conditions for removal of specific α-amino protecting groups may be used as described in Schroder & Lubke (1965).

[0041] After removal of the α-amino-protecting group, the remaining α-amino- and side chain-protected amino acids are coupled step-wise in the desired order to obtain the intermediate compound defined hereinbefore, or as an alternative to adding each amino acid separately in the synthesis, some of them may be coupled to one another prior to addition to the solid phase reactor. Selection of an appropriate coupling reagent is within the skill of the art. Particularly

suitable as a coupling reagent is N,N'-dicyclohexylcarbodiimide (DCC, DIC, HBTU, HATU, TBTU in the presence of HoBt or HoAt).

[0042] The activating reagents used in the solid phase synthesis of the peptides are well known in the peptide art. Examples of suitable activating reagents are carbodiimides, such as N,N'-diisopropylcarbodiimide and N-ethyl-N'-(3-dimethylaminopropyl)carbodiimide. Other activating reagents and their use in peptide coupling are described by Schroder & Lubke (1965) and Kapoor (1970).

[0043] Each protected amino acid or amino acid sequence is introduced into the solid-phase reactor in about a twofold or more excess, and the coupling may be carried out in a medium of dimethylformamide (DMF):CH_2Cl_2 (1:1) or in DMF or CH_2Cl_2 alone. In cases where intermediate coupling occurs, the coupling procedure is repeated before removal of the α-amino protecting group prior to the coupling of the next amino acid. The success of the coupling reaction at each stage of the synthesis, if performed manually, is preferably monitored by the ninhydrin reaction, as described by Kaiser et al. (1970). Coupling reactions can be performed automatically, as on a Beckman 990 automatic synthesizer, using a program such as that reported in Rivier et al. (1978).

[0044] After the desired amino acid sequence has been completed, the intermediate peptide can be removed from the resin support by treatment with a reagent, such as liquid hydrogen fluoride or TFA (if using Fmoc chemistry), which not only cleaves the peptide from the resin but also cleaves all remaining side chain protecting groups and also the -amino protecting group at the N-terminus if it was not previously removed to obtain the peptide in the form of the free acid. If Met is present in the sequence, the Boc protecting group is preferably first removed using trifluoroacetic acid (TFA)/ethanedithiol prior to cleaving the peptide from the resin with HF to eliminate potential S-alkylation. When using hydrogen fluoride or TFA for cleaving, one or more scavengers such as anisole, cresol, dimethyl sulfide and methylethyl sulfide are included in the reaction vessel.

[0045] Cyclization of the linear peptide is preferably affected, as opposed to cyclizing the peptide while a part of the peptido-resin, to create bonds between Cys residues. To effect such a disulfide cyclizing linkage, fully protected peptide can be cleaved from a hydroxymethylated resin or a chloromethylated resin support by ammonolysis, as is well known in the art, to yield the fully protected amide intermediate, which is thereafter suitably cyclized and deprotected. Alternatively, deprotection, as well as cleavage of the peptide from the above

resins or a benzhydrylamine (BHA) resin or a methylbenzhydrylamine (MBHA), can take place at 0°C with hydrofluoric acid (HF) or TFA, followed by oxidation as described above.

[0046] The peptides are also synthesized using an automatic synthesizer. Amino acids are sequentially coupled to an MBHA Rink resin (typically 100 mg of resin) beginning at the C-terminus using an Advanced Chemtech 357 Automatic Peptide Synthesizer. Couplings are carried out using 1,3-diisopropylcarbodimide in N-methylpyrrolidinone (NMP) or by 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (HBTU) and diethylisopropylethylamine (DIEA). The FMOC protecting group is removed by treatment with a 20% solution of piperidine in dimethylformamide(DMF). Resins are subsequently washed with DMF (twice), followed by methanol and NMP.

[0047] Muteins, analogs or active fragments, of the foregoing conotoxin peptides are also contemplated here. See, e.g., Hammerland et al. (1992). Derivative muteins, analogs or active fragments of the conotoxin peptides may be synthesized according to known techniques, including conservative amino acid substitutions, such as outlined in U.S. Patent Nos. 5,545,723 (see particularly col. 2, line 50--col. 3, line 8); 5,534,615 (see particularly col. 19, line 45--col. 22, line 33); and 5,364,769 (see particularly col. 4, line 55--col. 7, line 26), each herein incorporated by reference.

[0048] Pharmaceutical compositions containing a compound of the present invention as the active ingredient can be prepared according to conventional pharmaceutical compounding techniques. See, for example, *Remington's Pharmaceutical Sciences*, 18th Ed. (1990, Mack Publishing Co., Easton, PA). Typically, an antagonistic amount of active ingredient will be admixed with a pharmaceutically acceptable carrier. The carrier may take a wide variety of forms depending on the form of preparation desired for administration, e.g., intravenous, oral, parenteral or intrathecally. For examples of delivery methods see U.S. Patent No. 5,844,077, incorporated herein by reference.

[0049] "Pharmaceutical composition" means physically discrete coherent portions suitable for medical administration. "Pharmaceutical composition in dosage unit form" means physically discrete coherent units suitable for medical administration, each containing a daily dose or a multiple (up to four times) or a sub-multiple (down to a fortieth) of a daily dose of the active compound in association with a carrier and/or enclosed within an envelope. Whether the composition contains a daily dose, or for example, a half, a third or a quarter of a daily dose, will

depend on whether the pharmaceutical composition is to be administered once or, for example, twice, three times or four times a day, respectively.

[0050] The term "salt", as used herein, denotes acidic and/or basic salts, formed with inorganic or organic acids and/or bases, preferably basic salts. While pharmaceutically acceptable salts are preferred, particularly when employing the compounds of the invention as medicaments, other salts find utility, for example, in processing these compounds, or where non-medicament-type uses are contemplated. Salts of these compounds may be prepared by art-recognized techniques.

[0051] Examples of such pharmaceutically acceptable salts include, but are not limited to, inorganic and organic addition salts, such as hydrochloride, sulphates, nitrates or phosphates and acetates, trifluoroacetates, propionates, succinates, benzoates, citrates, tartrates, fumarates, maleates, methane-sulfonates, isothionates, theophylline acetates, salicylates, respectively, or the like. Lower alkyl quaternary ammonium salts and the like are suitable, as well.

[0052] As used herein, the term "pharmaceutically acceptable" carrier means a non-toxic, inert solid, semi-solid liquid filler, diluent, encapsulating material, formulation auxiliary of any type, or simply a sterile aqueous medium, such as saline. Some examples of the materials that can serve as pharmaceutically acceptable carriers are sugars, such as lactose, glucose and sucrose, starches such as corn starch and potato starch, cellulose and its derivatives such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt, gelatin, talc; excipients such as cocoa butter and suppository waxes; oils such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; glycols, such as propylene glycol, polyols such as glycerin, sorbitol, mannitol and polyethylene glycol; esters such as ethyl oleate and ethyl laurate, agar; buffering agents such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline, Ringer's solution; ethyl alcohol and phosphate buffer solutions, as well as other non-toxic compatible substances used in pharmaceutical formulations.

[0053] Wetting agents, emulsifiers and lubricants such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, releasing agents, coating agents, sweetening, flavoring and perfuming agents, preservatives and antioxidants can also be present in the composition, according to the judgment of the formulator. Examples of pharmaceutically acceptable antioxidants include, but are not limited to, water soluble antioxidants such as ascorbic acid, cysteine hydrochloride, sodium bisulfite, sodium metabisulfite, sodium sulfite,

and the like; oil soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, aloha-tocopherol and the like; and the metal chelating agents such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid and the like.

[0054] For oral administration, the compounds can be formulated into solid or liquid preparations such as capsules, pills, tablets, lozenges, melts, powders, suspensions or emulsions. In preparing the compositions in oral dosage form, any of the usual pharmaceutical media may be employed, such as, for example, water, glycols, oils, alcohols, flavoring agents, preservatives, coloring agents, suspending agents, and the like in the case of oral liquid preparations (such as, for example, suspensions, elixirs and solutions); or carriers such as starches, sugars, diluents, granulating agents, lubricants, binders, disintegrating agents and the like in the case of oral solid preparations (such as, for example, powders, capsules and tablets). Because of their ease in administration, tablets and capsules represent the most advantageous oral dosage unit form, in which case solid pharmaceutical carriers are obviously employed. If desired, tablets may be sugar-coated or enteric-coated by standard techniques. The active agent can be encapsulated to make it stable to passage through the gastrointestinal tract while at the same time allowing for passage across the blood brain barrier. See for example, WO 96/11698.

[0055] For parenteral administration, the compound may be dissolved in a pharmaceutical carrier and administered as either a solution or a suspension. Illustrative of suitable carriers are water, saline, dextrose solutions, fructose solutions, ethanol, or oils of animal, vegetative or synthetic origin. The carrier may also contain other ingredients, for example, preservatives, suspending agents, solubilizing agents, buffers and the like. When the compounds are being administered intrathecally, they may also be dissolved in cerebrospinal fluid.

[0056] A variety of administration routes are available. The particular mode selected will depend of course, upon the particular drug selected, the severity of the disease state being treated and the dosage required for therapeutic efficacy. The methods of this invention, generally speaking, may be practiced using any mode of administration that is medically acceptable, meaning any mode that produces effective levels of the active compounds without causing clinically unacceptable adverse effects. Such modes of administration include oral, rectal, sublingual, topical, nasal, transdermal or parenteral routes. The term "parenteral" includes subcutaneous, intravenous, epidural, irrigation, intramuscular, release pumps, or infusion.

[0057] For example, administration of the active agent according to this invention may be achieved using any suitable delivery means, including:

(a) pump (see, e.g., Luer & Hatton (1993), Zimm et al. (1984) and Ettinger et al. (1978));

(b), microencapsulation (see, e.g., U.S. Patent Nos. 4,352,883; 4,353,888; and 5,084,350);

(c) continuous release polymer implants (see, e.g., U.S. Patent No. 4,883,666);

(d) macroencapsulation (see, e.g., U.S. Patent Nos. 5,284,761, 5,158,881, 4,976,859 and 4,968,733 and published PCT patent applications WO92/19195, WO 95/05452);

(e) naked or unencapsulated cell grafts to the CNS (see, e.g., U.S. Patent Nos. 5,082,670 and 5,618,531);

(f) injection, either subcutaneously, intravenously, intra-arterially, intramuscularly, or to other suitable site; or

(g) oral administration, in capsule, liquid, tablet, pill, or prolonged release formulation.

[0058] In one embodiment of this invention, an active agent is delivered directly into the CNS, preferably to the brain ventricles, brain parenchyma, the intrathecal space or other suitable CNS location, most preferably intrathecally.

[0059] Alternatively, targeting therapies may be used to deliver the active agent more specifically to certain types of cell, by the use of targeting systems such as antibodies or cell specific ligands. Targeting may be desirable for a variety of reasons, e.g. if the agent is unacceptably toxic, or if it would otherwise require too high a dosage, or if it would not otherwise be able to enter the target cells.

[0060] The active agents, which are peptides, can also be administered in a cell based delivery system in which a DNA sequence encoding an active agent is introduced into cells designed for implantation in the body of the patient, especially in the spinal cord region. Suitable delivery systems are described in U.S. Patent No. 5,550,050 and published PCT Application Nos. WO 92/19195, WO 94/25503, WO 95/01203, WO 95/05452, WO 96/02286, WO 96/02646, WO 96/40871, WO 96/40959 and WO 97/12635. Suitable DNA sequences can be prepared synthetically for each active agent on the basis of the developed sequences and the known genetic code.

[0061] Exemplary methods for administering such muscle relaxant compounds (e.g., so as to achieve sterile or aseptic conditions) will be apparent to the skilled artisan. Certain methods suitable for administering compounds useful according to the present invention are set

forth in Goodman and Gilman's *The Pharmacological Basis of Therapeutics*, 7th Ed. (1985). The administration to the patient can be intermittent; or at a gradual, continuous, constant or controlled rate. Administration can be to a warm-blooded animal (e.g. a mammal, such as a mouse, rat, cat, rabbit, dog, pig, cow or monkey); but advantageously is administered to a human being. Administration occurs after general anesthesia is administered. The frequency of administration normally is determined by an anesthesiologist, and typically varies from patient to patient.

[0062] The active agent is preferably administered in an therapeutically effective amount. By a "therapeutically effective amount" or simply "effective amount" of an active compound is meant a sufficient amount of the compound to treat the desired condition at a reasonable benefit/risk ratio applicable to any medical treatment. The actual amount administered, and the rate and time-course of administration, will depend on the nature and severity of the condition being treated. Prescription of treatment, e.g. decisions on dosage, timing, etc., is within the responsibility of general practitioners or spealists, and typically takes account of the disorder to be treated, the condition of the individual patient, the site of delivery, the method of administration and other factors known to practitioners. Examples of techniques and protocols can be found in *Remington's Parmaceutical Sciences*.

[0063] Dosage may be adjusted appropriately to achieve desired drug levels, locally or systemically. Typically the active agents of the present invention exhibit their effect at a dosage range from about 0.001 mg/kg to about 250 mg/kg, preferably from about 0.01 mg/kg to about 100 mg/kg of the active ingredient, more preferably from a bout 0.05 mg/kg to about 75 mg/kg. A suitable dose can be administered in multiple sub-doses per day. Typically, a dose or sub-dose may contain from about 0.1 mg to about 500 mg of the active ingredient per unit dosage form. A more preferred dosage will contain from about 0.5 mg to about 100 mg of active ingredient per unit dosage form. Dosages are generally initiated at lower levels and increased until desired effects are achieved. In the event that the response in a subject is insufficient at such doses, even higher doses (or effective higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits. Continuous dosing over, for example 24 hours or multiple doses per day are contemplated to achieve appropriate systemic levels of compounds.

[0064] Advantageously, the compositions are formulated as dosage units, each unit being adapted to supply a fixed dose of active ingredients. Tablets, coated tablets, capsules, ampoules and suppositories are examples of dosage forms according to the invention.

[0065] It is only necessary that the active ingredient constitute an effective amount, i.e., such that a suitable effective dosage will be consistent with the dosage form employed in single or multiple unit doses. The exact individual dosages, as well as daily dosages, are determined according to standard medical principles under the direction of a physician or veterinarian for use humans or animals.

[0066] The pharmaceutical compositions will generally contain from about 0.0001 to 99 wt. %, preferably about 0.001 to 50 wt. %, more preferably about 0.01 to 10 wt.% of the active ingredient by weight of the total composition. In addition to the active agent, the pharmaceutical compositions and medicaments can also contain other pharmaceutically active compounds. Examples of other pharmaceutically active compounds include, but are not limited to, analgesic agents, cytokines and therapeutic agents in all of the major areas of clinical medicine. When used with other pharmaceutically active compounds, the conopeptides of the present invention may be delivered in the form of drug cocktails. A cocktail is a mixture of any one of the compounds useful with this invention with another drug or agent. In this embodiment, a common administration vehicle (e.g., pill, tablet, implant, pump, injectable solution, etc.) would contain both the instant composition in combination supplementary potentiating agent. The individual drugs of the cocktail are each administered in therapeutically effective amounts. A therapeutically effective amount will be determined by the parameters described above; but, in any event, is that amount which establishes a level of the drugs in the area of body where the drugs are required for a period of time which is effective in attaining the desired effects.

[0067] The present invention also relates to rational drug design for the indentification of additional drugs which can be used for the pursposes described herein. The goal of rational drug design is to produce structural analogs of biologically active polypeptides of interest or of small molecules with which they interact (e.g., agonists, antagonists, inhibitors) in order to fashion drugs which are, for example, more active or stable forms of the polypeptide, or which, e.g., enhance or interfere with the function of a polypeptide *in vivo*. Several approaches for use in rational drug design include analysis of three-dimensional structure, alanine scans, molecular modeling and use of anti-id antibodies. These techniques are well known to those skilled in the art. Such techniques may include providing atomic coordinates defining a three-dimensional

structure of a protein complex formed by said first polypeptide and said second polypeptide, and designing or selecting compounds capable of interfering with the interaction between a first polypeptide and a second polypeptide based on said atomic coordinates.

[0068] Following identification of a substance which modulates or affects polypeptide activity, the substance may be further investigated. Furthermore, it may be manufactured and/or used in preparation, i.e., manufacture or formulation, or a composition such as a medicament, pharmaceutical composition or drug. These may be administered to individuals.

[0069] A substance identified as a modulator of polypeptide function may be peptide or non-peptide in nature. Non-peptide "small molecules" are often preferred for many *in vivo* pharmaceutical uses. Accordingly, a mimetic or mimic of the substance (particularly if a peptide) may be designed for pharmaceutical use.

[0070] The designing of mimetics to a known pharmaceutically active compound is a known approach to the development of pharmaceuticals based on a "lead" compound. This approach might be desirable where the active compound is difficult or expensive to synthesize or where it is unsuitable for a particular method of administration, e.g., pure peptides are unsuitable active agents for oral compositions as they tend to be quickly degraded by proteases in the alimentary canal. Mimetic design, synthesis and testing is generally used to avoid randomly screening large numbers of molecules for a target property.

[0071] Once the pharmacophore has been found, its structure is modeled according to its physical properties, e.g., stereochemistry, bonding, size and/or charge, using data from a range of sources, e.g., spectroscopic techniques, x-ray diffraction data and NMR. Computational analysis, similarity mapping (which models the charge and/or volume of a pharmacophore, rather than the bonding between atoms) and other techniques can be used in this modeling process.

[0072] A template molecule is then selected, onto which chemical groups that mimic the pharmacophore can be grafted. The template molecule and the chemical groups grafted thereon can be conveniently selected so that the mimetic is easy to synthesize, is likely to be pharmacologically acceptable, and does not degrade *in vivo*, while retaining the biological activity of the lead compound. Alternatively, where the mimetic is peptide-based, further stability can be achieved by cyclizing the peptide, increasing its rigidity. The mimetic or mimetics found by this approach can then be screened to see whether they have the target

property, or to what extent it is exhibited. Further optimization or modification can then be carried out to arrive at one or more final mimetics for *in vivo* or clinical testing.

[0073] The present invention further relates to the use of a labeled (e.g., radiolabel, fluorophore, chromophore or the like) of the conotoxins described herein as a molecular tool both *in vitro* and *in vivo*, for discovery of small molecules that exert their action at or partially at the same functional site as the native toxin and capable of elucidation similar functional responses as the native toxin. In one embodiment, the displacement of a labeled conotoxin from its receptor or other complex by a candidate drug agent is used to identify suitable candidate drugs. In a second embodiment, a biological assay on a test compound to determine the therapeutic activity is conducted and compared to the results obtained from the biological assay of a conotoxin. In a third embodiment, the binding affinity of a small molecule to the receptor of a conotoxin is measured and compared to the binding affinity of a conotoxin to its receptor.

[0074] The practice of the present invention employs, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, genetics, immunology, cell biology, cell culture and transgenic biology, which are within the skill of the art. See, e.g., Maniatis *et al.*, 1982; Sambrook *et al.*, 1989; Ausubel *et al.*, 1992; Glover, 1985; Anand, 1992; Guthrie and Fink, 1991; Harlow and Lane, 1988; Jakoby and Pastan, 1979; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); Riott, *Essential Immunology*, 6th Edition, Blackwell Scientific Publications, Oxford, 1988; Hogan et al., Manipulating the Mouse Embryo, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

EXAMPLES

[0075] The present invention is described by reference to the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner. Standard techniques well known in the art or the techniques specifically described below were utilized.

EXAMPLE 1

Isolation of Conotoxin Peptides

[0076] Crude venom was extracted from venom ducts (Cruz et al., 1976), and the components were purified as previously described (Cartier et al., 1996). The crude extract from venom ducts was purified by reverse phase liquid chromatography (RPLC) using a Vydac C_{18} semi-preparative column (10 x 250 mm). Further purification of bioactive peaks was done on a Vydac C_{18} analytical column (4.6 x 220 mm). The effluents were monitored at 220 nm. Peaks were collected, and aliquots were assayed for activity. Throughout purification, HPLC fractions were assayed by means of intracerebral ventricular (i.c.v.) injection into mice (Clark et al., 1981).

[0077] The amino acid sequence of the purified peptides were determined by standard methods. The purified peptides were reduced and alkylated prior to sequencing by automated Edman degradation on an Applied Biosystems 477A Protein Sequencer with a 120A Analyzer (DNA/Peptide Facility, University of Utah) (Martinez et al., 1995; Shon et al., 1994).

[0078] In accordance with this method, the conotoxin peptides described as "isolated" in Table 1 were obtained. These conotoxin peptides, as well as the other conotoxin peptides and the conotoxin peptide precursors set forth in Table 1 are synthesized as described in U.S. Patent No. 5,670,622.

EXAMPLE 2

Isolation of DNA Encoding Conopeptides

[0079] DNA coding for conotoxin peptides was isolated and cloned in accordance with conventional techniques using general procedures well known in the art, such as described in Olivera et al. (1996), including using primers based on the DNA sequence of known conotoxin peptides. For example, primers based on the DNA sequence for the Contulakin-G propeptide were used to identify contulakin homologs. The propeptides of these contulakin homologs are

homologous on the basis of primer amplification, even though the sequence of the mature toxins are not homologous with the Contulakin-G mature toxin. Alternatively, cDNA libraries was prepared from *Conus* venom duct using conventional techniques. DNA from single clones was amplified by conventional techniques using primers which correspond approximately to the M13 universal priming site and the M13 reverse universal priming site. Clones having a size of approximately 300-500 nucleotides were sequenced and screened for similarity in sequence to known conotoxins. The DNA sequences and encoded propeptide sequences are set forth in Table 1. DNA sequences coding for the mature toxin can also be prepared on the basis of the DNA sequences set forth in Table1. An alignment of the conopeptides of the present invention is set forth in Tables 2-14.

TABLE 1

Name: Af6.1
Species: ammiralis
Cloned: Yes

DNA Sequence:
ATCATGGAGAAACTGATAATTCTGCTTCTTGTTGCTGCTGTACTGATGTCGACCCAG
GCCCTGGTTGAACGTGCTGGAGAAAACCGCTCAAAGGAGAACATCAATTTTTATT
AAAAAGAAAGAGAGCTGCTGACAGGGGGATGTGGGCGATTGCAAAGATGGGTTA
ACGACATGTTTTGCGCCCTCAGAGTGTTGTTCTGAGGATTGTGAAGGGAGCTGCACG
ATGTGGTGATGACCTCTGACCACAAGCCATCTGACATCACCACTCTCCTCTTCAGAG
GCTTCAAG (SEQ ID NO:1)

Translation:
MEKLIILLLVAAVLMSTQALVERAGENRSKENINFLLKRKRAADRGMWGDCKDGLTTC
FAPSECCSEDCEGSCTMW (SEQ ID NO:2)

Toxin Sequence:
Gly-Met-Xaa4-Gly-Asp-Cys-Lys-Asp-Gly-Leu-Thr-Thr-Cys-Phe-Ala-Xaa3-Ser-Xaa1-Cys-Cys-Ser-Xaa1-Asp-Cys-Xaa1-Gly-Ser-Cys-Thr-Met-Xaa4-^ (SEQ ID NO:3)

Name: Af6.2
Species: ammiralis
Cloned: Yes

DNA Sequence:
ATCATGGAGAAACTGACAATTCTGCTTCTTGTTGCTGCTGTACTGATGTCGACCCAG
GCCCTGCCTCAAGGTGGTGGAGAAAAACGCCCAAGGGAGAATATCAGATTTTTATC
AAAAAGAAAGACAAATGCTGAGCGTTGGAGGGAGGGCAGTTGCACCTCTTGGTTAG

CGACGTGTACGCAAGACCAGCAATGCTGTACTGATGTTTGTTACAAAAGGGACTAC
TGCGCCTTGTGGGATGACCGCTGACCACAAGCCATCTGACATCACCACTCTCCTGTT
CAGAGTCTTCAAG (SEQ ID NO:4)

Translation:
MEKLTILLLVAAVLMSTQALPQGGGEKRPRENIRFLSKRKTNAERWREGSCTSWLATC
TQDQQCCTDVCYKRDYCALWDDR (SEQ ID NO:5)

Toxin Sequence:
Xaa4-Arg-Xaa1-Gly-Ser-Cys-Thr-Ser-Xaa4-Leu-Ala-Thr-Cys-Thr-Gln-Asp-Gln-Gln-Cys-Cys-Thr-Asp-Val-Cys-Xaa5-Lys-Arg-Asp-Xaa5-Cys-Ala-Leu-Xaa4-Asp-Asp-Arg-^ (SEQ ID NO:6)

Name: Af6.3
Species: ammiralis
Cloned: Yes

DNA Sequence:
ATCATGCAGAAACTGATAATTCTGCTTCTTGTTGCTGCTGTGCTGATGTCGACCCAG
GCCCTGTTTCAAGAAAAACGCACAATGAAGAAGATCGATTTTTTATCAAAGGGAAA
GGCAGATGCTGAGAAGCAGAGGAAGCGCAATTGCTCGGATGATTGGCAGTATTGTG
AAAGTCCCAGTGACTGCTGTAGTTGGGATTGTGATGTGGTCTGCTCGGGATGAACTC
TGACCACAAGTCATCCGACATCACCACTCTCCTGTTCAGAGGCTTCAAG (SEQ ID NO:7)

Translation:
MQKLIILLLVAAVLMSTQALFQEKRTMKKIDFLSKGKADAEKQRKRNCSDDWQYCESP
SDCCSWDCDVVCSG (SEQ ID NO:8

Toxin Sequence:
Asn-Cys-Ser-Asp-Asp-Xaa4-Gln-Xaa5-Cys-Xaa1-Ser-Xaa3-Ser-Asp-Cys-Cys-Ser-Xaa4-Asp-Cys-Asp-Val-Val-Cys-Ser-# (SEQ ID NO:9)

Name: Af6.4
Species: ammiralis
Cloned: Yes

DNA Sequence:
ATCATGCAGAAACTGATAATCCTGCTTCTTGTTGCTGCTCTACTGTTGTCGATCCAG
GCGGTAAATCAAGAAAAACACCAACGGGCAAAGATCAACTTGCTTTCAAAGAGAA
AGCCACCTGCTGAGCGTTGGTGGCGGTGGGGAGGATGCATGGCTTGGTTTGGGAAA
TGTTCGAAGGACTCGGAATGTTGTTCTAATAGTTGTGACATAACGCGCTGCGAGTTA
ATGCGATTCCCACCAGACTGGTGACATCGACACTCTCCTGTTCAGAGTCTTCAAG
(SEQ ID NO:10)

Translation:

MQKLIILLLVAALLLSIQAVNQEKHQRAKINLLSKRKPPAERWWRWGGCMAWFGKCS
KDSECCSNSCDITRCELMRFPPDW (SEQ ID NO:11)

Toxin Sequence:

Xaa4-Xaa4-Arg-Xaa4-Gly-Gly-Cys-Met-Ala-Xaa4-Phe-Gly-Lys-Cys-Ser-Lys-Asp-Ser-Xaa1-Cys-Cys-Ser-Asn-Ser-Cys-Asp-Ile-Thr-Arg-Cys-Xaa1-Leu-Met-Arg-Phe-Xaa3-Xaa3-Asp-Xaa4-^ (SEQ ID NO:12)

Name: Af6.5
Species: ammiralis
Cloned: Yes

DNA Sequence:

ATCATGGAGAAACTGACAATCCTGCTTCTTGTTGCTGCTGTACTGACGTCGACCCAG
GCCCTGATTCAAGGTGGTGGAGACGAACGCCAAAAGGCAAAGATCAACTTTCTTTC
AAGGTCGGACCGCGATTGCAGGGGTTACGATGCGCCGTGTAGCTCTGGCGCGCCAT
GTTGTGATTGGTGGACATGTTCAGCACGAACCGGGCGCTGTTTTTAGGCTGACCACA
AGCCATCCGACATCACCACTCTCCTCTTCAGAGGCTTCAAG (SEQ ID NO:13)

Translation:

MEKLTILLLVAAVLTSTQALIQGGGDERQKAKINFLSRSDRDCRGYDAPCSSGAPCCDW
WTCSARTGRCF (SEQ ID NO:14)

Toxin Sequence:

Asp-Cys-Arg-Gly-Xaa5-Asp-Ala-Xaa3-Cys-Ser-Ser-Gly-Ala-Xaa3-Cys-Cys-Asp-Xaa4-Xaa4-Thr-Cys-Ser-Ala-Arg-Thr-Gly-Arg-Cys-Phe-^ (SEQ ID NO:15)

Name: Af6.6
Species: ammiralis
Cloned: Yes

DNA Sequence:

ATCATGCAGAAACTGACAATTCTGCTTCTTGTTGCTGCTGTGCTGATGTCGACCCAG
GCCGTGCTTCAAGAAAAACGCCCAAAGGAGAAGATCAAGTTTTTATCAAAGAAAAA
GACAGATGCTGAGAAGCAGCAGAAGCGCCTTTGCCCGGATTACACGGAGCCTTGTT
CACATGCCCATGAATGCTGTTCATGGAATTGTCATAATGGGCACTGCACGGGATGA
ACTCGGACCACAAGCCATCGACATCATCACTCTCCTGTTCAGAGTCTTCAAG (SEQ ID NO:16)

Translation:

MQKLTILLLVAAVLMSTQAVLQEKRPKEKIKFLSKKKTDAEKQQKRLCPDYTEPCSHA
HECCSWNCHNGHCTG (SEQ ID NO:17)

Toxin Sequence:

Leu-Cys-Xaa3-Asp-Xaa5-Thr-Xaa1-Xaa3-Cys-Ser-His-Ala-His-Xaa1-Cys-Cys-Ser-Xaa4-Asn-Cys-His-Asn-Gly-His-Cys-Thr-# (SEQ ID NO:18)

Name: Af6.7
Species: ammiralis
Cloned: Yes

DNA Sequence:
ATCATGCAGAAACTGATAATTCTGCTCCTTGTTGCTGCTGTACTGATGTCGACCCAG
GCCATGTTTCAAGGTGATGGAGAAAAATCCCGGAAAGCGGAGATCAACTTTTCTAA
AACAAGAAATTTGGCGAGAAACAAGCAGAAACGCTGCAGTAGTTGGGCAAAGTATT
GTGAAGTTGACTCGGAATGCTGTTCCGAACAGTGTGTAAGGTCTTACTGCGCGATGT
GGTGATGACCTCTGACCACAAGCCATCCGATATCACCACTCTCCTCTTCAGAGACTT
CAAG (SEQ ID NO:19)

Translation:
MQKLIILLLVAAVLMSTQAMFQGDGEKSRKAEINFSKTRNLARNKQKRCSSWAKYCEV
DSECCSEQCVRSYCAMW (SEQ ID NO:20)

Toxin Sequence:
Cys-Ser-Ser-Xaa4-Ala-Lys-Xaa5-Cys-Xaa1-Val-Asp-Ser-Xaa1-Cys-Cys-Ser-Xaa1-Gln-Cys-Val-Arg-Ser-Xaa5-Cys-Ala-Met-Xaa4-^ (SEQ ID NO:21)

Name: Af9.1
Species: ammiralis
Cloned: Yes

DNA Sequence:
GTTAAAATGCATCTGTCACTGGCACGCTCAGCTGTTTTGATGTTGCTTCTGCTGTTTG
CCTTGGGCAACTTTGTTGTGGTCCAGTCAGGACAGATAACAAGAGATGTGGACAAT
GGACAGCTCACGGACAACCGCCGTAACCTGCAATCGAAGTGGAAGCCAGTGAGTCT
CTTCATGTCACGACGGTCTTGTAACAATTCTTGCAATGAGCATTCCGATTGCGAATC
CCATTGTATTTGCACGTTTAGCGGATGCAAAATTATTTTGATATAAACGGATTGAGT
TTGCTCGTCAACAAGATGTCGCACTACAGCTCCTCTCTACAGTGTGTACATCGACCA
AACGACGCATCTTTTATTTCTTTGTCTGTTGTATTTGTTTTCCTGTGTTCATAACGTAC
AGAGCCCTTTAATTACCTTTACTGCTCTTCACTTAACCTGATAACCGGAAGGTCCAG
TGCT (SEQ ID NO:22)

Translation:
MHLSLARSAVLMLLLLFALGNFVVVQSGQITRDVDNGQLTDNRRNLQSKWKPVSLFM
SRRSCNNSCNEHSDCESHCICTFSGCKIILI (SEQ ID NO:23)

Toxin Sequence:
Ser-Cys-Asn-Asn-Ser-Cys-Asn-Xaa1-His-Ser-Asp-Cys-Xaa1-Ser-His-Cys-Ile-Cys-Thr-Phe-Ser-Gly-Cys-Lys-Ile-Ile-Leu-Ile-^ (SEQ ID NO:24)

Name: Af9.2
Species: ammiralis
Cloned: Yes

DNA Sequence:
GTTAAAATGCATCTGTCACTGGCACGCTTAGCTGTTTTGATGTTGCTTCTGCTGTTTG
CCTTGGGCAACTTTGTTGTGGTCCAGTCAGGACAGATAACAAGAGATGTGGACAAT
GGACAGCTCACGGACAACCGCCGTAACCTGCAATCGAAGTGGAAGCCAGTGAGTCT
CTTCATGTCACGACGGTCTTGTAACAATTCTTGCAATGAGCATTCCGATTGCGAATC
CCATTGTATTTGCACGTTTAGAGGATGCGGAGCTGTTAATGGTTGAGTTTGCTCGTC
AACATGATGTCGCACTACACACTACAGCTCCTCTCTACAGTGTGTACATCGACCAAA
CGACGCATCTTTTATTTCTTTGTCTGTTGTGTTTGTTTTCCTGTGTTCATAACGTACAG
AGCCCTTTAATTACTTTTACTGCTCTTCACTTAACCTGATAACCAGAAGGTCCAGTG
CT (SEQ ID NO:25)

Translation:
MHLSLARLAVLMLLLLFALGNFVVVQSGQITRDVDNGQLTDNRRNLQSKWKPVSLFM
SRRSCNNSCNEHSDCESHCICTFRGCGAVNG (SEQ ID NO:26)

Toxin Sequence:
Ser-Cys-Asn-Asn-Ser-Cys-Asn-Xaa1-His-Ser-Asp-Cys-Xaa1-Ser-His-Cys-Ile-Cys-Thr-Phe-Arg-Gly-Cys-Gly-Ala-Val-Asn-# (SEQ ID NO:27)

Name: Ar6.1
Species: arenatus
Cloned: Yes

DNA Sequence:
ACCAAAACCATCATCAAAATGAAACTGACGTGCGTGGTGATCGTCGCTGTGCTGTTC
CTGACGGCCTGTCAACTCACTACAGCTGATGACTCCAGAGGTACGCAGAAGCATGG
TGCCCTGAGATCGACCACCAAACTCTCCATGTTGACTCGGGGCTGCACGCCTCCTGG
TGGAGTTTGTGGTTATCATGGTCACTGCTGCGATTTTTGCGATACGTTCGGCAATTTA
TGTGTGAGTGGCTGACCCGGCATCTGACCTTTCCCCCTTCTTTGCTCCACTATCCTTT
TTCTGCCTGAGTCCTCCATACCTGAGAGCTGTCATGAACCACTCAACACCTACTCTT
CCGGAGGTTTCTGAGGAGCTGCATTGAAATAAAAGCCGCATTGC (SEQ ID NO:28)

Translation:
MKLTCVVIVAVLFLTACQLTTADDSRGTQKHGALRSTTKLSMLTRGCTPPGGVCGYHG
HCCDFCDTFGNLCVSG (SEQ ID NO:29)

Toxin Sequence:
Gly-Cys-Thr-Xaa3-Xaa3-Gly-Gly-Val-Cys-Gly-Xaa5-His-Gly-His-Cys-Cys-Asp-Phe-Cys-Asp-Thr-Phe-Gly-Asn-Leu-Cys-Val-Ser-# (SEQ ID NO:30)

Name: Bromosleeper-Ar1
Species: arenatus
Cloned: Yes

DNA Sequence:
GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCTT
CTACTTCTTGTGTTCATGGCAACCAGTCATCAGGATGCAGGAGAGAAGAAGGCGAT
GCAAAGGGACGCAATCAACGTCAGACGGAGAAGATCACTCACTCGGGGAGTAGTA
ACTGAGGCGTGCGAAGAGTCCTGTGAGGAGGAGGAAAAGCACTGCTGCCACGTAA
ATAATGGAGTACCCTCTTGTGCCGTTATATGCTGGGGATAGTTTCTCGCACACTGTC
TCATTCATTATTTTATCAGTACAAGTGTAAACGAGACATGTCAGAAAGTCGAAGGTT
GTGCGTATTTGATAAGTATTGTTTACTGGGATGAACGGA (SEQ ID NO:31)

Translation:
MSGLGIMVLTLLLLVFMATSHQDAGEKKAMQRDAINVRRRRSLTRGVVTEACEESCEE
EEKHCCHVNNGVPSCAVICWG (SEQ ID NO:32)

Toxin Sequence:
Val-Val-Thr-Xaa1-Ala-Cys-Xaa1-Xaa1-Ser-Cys-Xaa1-Xaa1-Xaa1-Xaa1-Lys-His-Cys-Cys-His-
Val-Asn-Asn-Gly-Val-Xaa3-Ser-Cys-Ala-Val-Ile-Cys-Xaa4-# (SEQ ID NO:33)

Name: Bromosleeper-Ar1A
Species: arenatus
Cloned: Yes

DNA Sequence:
GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCTT
CTACTTCTTGTGTTCATGGCAACCAGTCATCAGGATGCAGGAGAGAAGCAGGCGAC
GGAAAGGGACGCAATCAACATCAGATGGAGAAGATCACGCACTCGGAGAATAGTA
ACTGAGGCGTGCGAAGAGTCCTGTGAGGACGAGGAAAAGCACTGCTGCCACGTAA
ATAATGGAGTACCCTCTTGTGCCGTTATATGCTGGGGATAGTTTCTCGCACACTGTC
TCATTCATTATTTTATCAGTACAAGTGTAAACGAGACATGTCAGAAAGTCGAAGGTT
GTGCGTATTTGATAAGTATTGTTTACTGGGATGAACGGA (SEQ ID NO:34)

Translation:
MSGLGIMVLTLLLLVFMATSHQDAGEKQATERDAINIRWRRSRTRRIVTEACEESCEDE
EKHCCHVNNGVPSCAVICWG (SEQ ID NO:35)

Toxin Sequence:
Ile-Val-Thr-Xaa1-Ala-Cys-Xaa1-Xaa1-Ser-Cys-Xaa1-Asp-Xaa1-Xaa1-Lys-His-Cys-Cys-His-
Val-Asn-Asn-Gly-Val-Xaa3-Ser-Cys-Ala-Val-Ile-Cys-Xaa4-# (SEQ ID NO:36)

Name: Bromosleeper-Ar2
Species: arenatus
Cloned: Yes

DNA Sequence:
GACAGGATTGAACAAAATTCAGGATGTCAGAACTGGGAATCATGGTGCTAACGCTT CTACTTCTTGTGTTCCTGGTAACCAGTCATCAGGATGCAGGAGAGAAGCAGGCGAC GGAAAGGGACGCAATCAACATCAGATGGAGAAGATCACTCACTCGGAGAATAGTA ACTGAGGCGTGCGAAGAGCACTGTGAGGATGAGGAACAGTTCTGCTGCGGCTTAGA GAATGGACAACCCTTTTGTGCCCCTGTTTGCTTCGGATAGTTTCTGTACACTGTCTCA TTAATTATTTTATCAGTACAAGTGTAAACAAAACATGTCAGAAAGTCGAAGGTTGTG CGTATTTGATAAGTATTGTTTGCTGGGACGAACGGA (SEQ ID NO:37)

Translation:
MSELGIMVLTLLLLVFLVTSHQDAGEKQATERDAINIRWRRSLTRRIVTEACEEHCEDEE QFCCGLENGQPFCAPVCFG (SEQ ID NO:38)

Toxin Sequence:
Ile-Val-Thr-Xaa1-Ala-Cys-Xaa1-Xaa1-His-Cys-Xaa1-Asp-Xaa1-Xaa1-Gln-Phe-Cys-Cys-Gly-Leu-Xaa1-Asn-Gly-Gln-Xaa3-Phe-Cys-Ala-Xaa3-Val-Cys-Phe-# (SEQ ID NO:39)

Name: Bromosleeper-Ar3
Species: arenatus
Cloned: Yes

DNA Sequence:
GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCTT CTACTTCTTGTGTTCATGGCAACCAGTCATCAGGATGCAGGAGAGAAGAAGGTGAT GCAAAGGGACGCAATCAACGTCAGACGGAGAAGATCACGCACTCGGAGAGTAGTA ACTGGGGCGTGCGAAGAGCACTGTGAGGACGAGGAAAAGCACTGCTGCGGCTTAG AGAATGGACAACCCTTTTGTGCCCGTCTATGCTTAGGATAGTTTTCTGTACACTGTCT TATTCATTATTTTATCAGTACAAGTGAAAACAAAGCATGTCAGAAAGTCGAAGGTTG TGCGTATTTGATAAGTATTGTTTACTGGGATGAACGGA (SEQ ID NO:40)

Translation:
MSGLGIMVLTLLLLVFMATSHQDAGEKKVMQRDAINVRRRRSRTRRVVTGACEEHCE DEEKHCCGLENGQPFCARLCLG (SEQ ID NO:41)

Toxin Sequence:
Val-Val-Thr-Gly-Ala-Cys-Xaa1-Xaa1-His-Cys-Xaa1-Asp-Xaa1-Xaa1-Lys-His-Cys-Cys-Gly-Leu-Xaa1-Asn-Gly-Gln-Xaa3-Phe-Cys-Ala-Arg-Leu-Cys-Leu-# (SEQ ID NO:42)

Name: C. arenatus contryphan 1
Species: arenatus
Cloned: Yes

DNA Sequence:
ATGGGGAAACTGACAATACTGGTTCTTGTTGCTGCTGTACTGTTGTCGACCCAGGTC
ATGGTTCAAGGTGACGGAGATCAACCTGCAGCTCGCAATGCAGTGCCAAAAGACGA
TAACCCAGATGGAGCGAGTGGAAAGTTCATGAATGTTCTACGTCGGTCTGGATGTC
CGTGGCATCCTTGGTGTGGCTGATCGGAATCCACGATTGCAATGACAGCC (SEQ ID NO:43)

Translation:
MGKLTILVLVAAVLLSTQVMVQGDGDQPAARNAVPKDDNPDGASGKFMNVLRRSGCP
WHPWCG (SEQ ID NO:44)

Toxin Sequence:
Ser-Gly-Cys-Xaa3-Xaa4-His-Xaa3-Xaa4-Cys-# (SEQ ID NO:45)

Name: C. arenatus contryphan 1A
Species: arenatus
Cloned: Yes

DNA Sequence:
ATGGGGAAACTGACAATACTGGTTCTTGTTGCTGCTGTACTGTTGTCGACCCAGGTC
ATGGTTCAAGGTGACGGAGATCAACCTGCAGCTCGCAATGCAGTGCCAAAAGACGA
TAACCCAGATGGAGCGAGTGGAAAGTTCATGAATGTTCTACGTCGGTCTGGATGTC
CGTGGCGCCCTTGGTGTGGCTGATCGGAATCCACGATTGCAATGACAGCC (SEQ ID NO:46)

Translation:
MGKLTILVLVAAVLLSTQVMVQGDGDQPAARNAVPKDDNPDGASGKFMNVLRRSGCP
WRPWCG (SEQ ID NO:47)

Toxin Sequence:
Ala-Ser-Gly-Cys-Xaa3-Xaa4-Arg-Xaa3-Xaa4-Cys-# (SEQ ID NO:48)

Name: C. arenatus contryphan 2
Species: arenatus
Cloned: Yes

DNA Sequence:
ATGGGGAAACTGACAATACTGGTTCTTGTTGCTGCTGTACTGTTGTCGACCCAGGTC
ATGGTTCAAGGTGACGGAGATCAACCTGCAGGTCGAGATGCAGTTCCAAGAGACGA
TAACCCAGGTGGAACGAGTGGAAAGTTCATGAATGCTCTACGTCAATATGGATGTC
CGGTGGGTCTTTGGTGTGACTGATCAGAATCCACGATTGCAATGACAGCC (SEQ ID NO:49)

Translation:

MGKLTILVLVAAVLLSTQVMVQGDGDQPAGRDAVPRDDNPGGTSGKFMNALRQYGC
PVGLWCD (SEQ ID NO:50)

Toxin Sequence:
Xaa2-Xaa5-Gly-Cys-Xaa3-Val-Gly-Leu-Xaa4-Cys-Asp-^ (SEQ ID NO:51)

Name: C. arenatus contryphan 4
Species: arenatus
Cloned: Yes

DNA Sequence:
ATGGGGAAACTGACAATACTGGTTCTTGTTGCTGCTGTACTGTTGTCGACCCAGGTC
ATGTTTCGAGATCAACCTGCACGTCGTGATGCAGTGCCAAGAGACGATAGCCCAGA
TGGAATGAGTGGAGGGTTCATGAATGTCCCACGTCGGTCTGGATGTCCGTGGCAAC
CTTGGTGTGGCTGATCGGAATCCACGATTGCAATGACAGCC (SEQ ID NO:52)

Translation:
MGKLTILVLVAAVLLSTQVMFRDQPARRDAVPRDDSPDGMSGGFMNVPRRSGCPWQP
WCG (SEQ ID NO:53)

Toxin Sequence:
Ser-Gly-Cys-Xaa3-Xaa4-Gln-Xaa3-Xaa4-Cys-# (SEQ ID NO:54)

Name: Contryphan-Ar-1
Species: arenatus
Cloned: Yes

DNA Sequence:
ATGGGGAAACTGACAATACTGGTTCTTGTTGCTGCTGTACTGTTGTCGACCCAGGCC
ATGGTTCAAGATCAACCTGCAGGTCGAGATGCAGTTCCAAGAGACGATAACCCAGG
TGGAACGAGTGGAAAGTTCGTGAATGCTCAACGTCAATATGGATGTCCGCCGGGTC
TTTGGTGTCACTGATCAGAATCCACGATTGCAATGACAGCC (SEQ ID NO:55)

Translation:
MGKLTILVLVAAVLLSTQAMVQDQPAGRDAVPRDDNPGGTSGKFVNAQRQYGCPPGL
WCH (SEQ ID NO:56)

Toxin Sequence:
Xaa2-Xaa5-Gly-Cys-Xaa3-Xaa3-Gly-Leu-Xaa4-Cys-His-^ (SEQ ID NO:57)

Name: A10.1
Species: aurisiacus
Cloned: Yes

DNA Sequence:
ATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCATCCCTTCAG
ATCGTGCATCTGATGGCAGGAATGCCGCAGTCAACGAGAGAGCGCCTTGGCTGGTC
CCTTCGACAATCACGACTTGCTGTGGATATAATCCGGGGACAATGTGCCCTCCTTGC
AGGTGCGATAATACCTGTTAACCAAAAAAAAAAAAAAAAAAA (SEQ ID NO:58)

Translation:
MFTVFLLVVLATTVVSIPSDRASDGRNAAVNERAPWLVPSTITTCCGYNPGTMCPPCRC
DNTC (SEQ ID NO:59)

Toxin Sequence:
Ala-Xaa3-Xaa4-Leu-Val-Xaa3-Ser-Thr-Ile-Thr-Thr-Cys-Cys-Gly-Xaa5-Asn-Xaa3-Gly-Thr-
Met-Cys-Xaa3-Xaa3-Cys-Arg-Cys-Asp-Asn-Thr-Cys-^ (SEQ ID NO:60)

Name: Bn1.5
Species: bandanus
Cloned: Yes

DNA Sequence:
ATGCGCTGTCTCCCAGTCTTGATCATTCTTCTGCTGCTGACTGCATCTGCACCTGGCG
TTGATGTCCTACCGAAGACCGAAGATGATGTGCCCCTGTCATCTGTCTACGATAATA
CAAAGAGTATCCTACGAGGACTTCTGGACAAACGTGCTTGCTGTGGCTACAAGCTTT
GCTCACCATGTTAACCAGCATGAAGGATCC (SEQ ID NO:61)

Translation:
MRCLPVLIILLLLTASAPGVDVLPKTEDDVPLSSVYDNTKSILRGLLDKRACCGYKLCSP
C (SEQ ID NO:62)

Toxin Sequence:
Ala-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-Ser-Xaa3-Cys-^ (SEQ ID NO:63)

Name: Ca6.3
Species: caracteristicus
Cloned: Yes

DNA Sequence:
GGATCCATGAAACTGACGTGCGTGGTGATCATCGCCGCGCTGTTCCTGACGGCCTGT
CAGCTCAATACAGCTGATGACTCCAGAGATAAGCAGGAGTACCGTGCAGTGAGGTT
GAGAGACGGAATGCGGAATTTCAAAGGTTCCAAGCGCAACTGCGGGGAACAAGGT
GAAGGTTGTGCTACTCGCCCATGCTGCTCTGGTCTGAGTTGCGTTGGCAGCCGTCCA
GGAGGCCTGTGCCAGTACGGCTAATAGTCTGGCATCTGATATTTCCCCTCTGCACTC
TACCTTCTTTTGCCTGATGCATGTTTACTTGTGTGTGGTCATGAACCACTCAGTAGCT
ACACCTCCGAAGGACGTGC (SEQ ID NO:64)

Translation:
MKLTCVVIIAALFLTACQLNTADDSRDKQEYRAVRLRDGMRNFKGSKRNCGEQGEGC
ATRPCCSGLSCVGSRPGGLCQYG (SEQ ID NO:65)

Toxin Sequence:
Asn-Cys-Gly-Xaa1-Gln-Gly-Xaa1-Gly-Cys-Ala-Thr-Arg-Xaa3-Cys-Cys-Ser-Gly-Leu-Ser-Cys-Val-Gly-Ser-Arg-Xaa3-Gly-Gly-Leu-Cys-Gln-Xaa5-# (SEQ ID NO:66)

Name: Ca8.1
Species: caracteristicus
Cloned: Yes

DNA Sequence:
ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCATCCTGCCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCTGAAGAGAGGCTTCTA
CGGTACTCTGGCAATGTCTACCAGAGGATGCTCTGGCACTTGCCATCGTCGTGAGGA
CGGCAAGTGTCGGGGTACTTGCGACTGCTCCGGATACAGCTATTGTCGCTGCGGTGA
CGCTCACCATTTTTACCGAGGATGCACGTGTTCGTGTCAAGGTTGATTAATTGACTC
TTTTAACTCGTTGAACGATTGAAAAAAAAAAATTTTAGAGCAATATGTTCGAGAAAA
ACCGAAGAC (SEQ ID NO:67)

Translation:
MMSKMGAMFVLLLLFILPSSQQEGDVQARKTHLKRGFYGTLAMSTRGCSGTCHRRED
GKCRGTCDCSGYSYCRCGDAHHFYRGCTCSCQG (SEQ ID NO:68)

Toxin Sequence:
Gly-Cys-Ser-Gly-Thr-Cys-His-Arg-Arg-Xaa1-Asp-Gly-Lys-Cys-Arg-Gly-Thr-Cys-Asp-Cys-Ser-Gly-Xaa5-Ser-Xaa5-Cys-Arg-Cys-Gly-Asp-Ala-His-His-Phe-Xaa5-Arg-Gly-Cys-Thr-Cys-Ser-Cys-Gln-# (SEQ ID NO:69)

Name: Ca8.2
Species: caracteristicus
Cloned: Yes

DNA Sequence:
ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCATCCTGCCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCGGAAGAGCGGCTTCTA
CGGTACTCTGGCAATGTCTGCCAGAGGATGCTCTGGCACTTGCCATCGTCGTGAGGA
CGGCAAGTGTCGGGGTACTTGCGACTGCTCCGGATACAGCTATTGTCGCTGCGGTGA
CGCTCACCATTTTTACCGAGGATGCACGTGTACATGTTAAGGTTGATTAATTGACTC
TTTTAACTCGTTGAACCGATTAAAAAAAAAAATTAGACGAATATGTTCGAGAAAACC
GAAGAC (SEQ ID NO:70)

Translation:

MMSKMGAMFVLLLLFILPSSQQEGDVQARKTHRKSGFYGTLAMSARGCSGTCHRRED
GKCRGTCDCSGYSYCRCGDAHHFYRGCTCTC (SEQ ID NO:71)

Toxin Sequence:

Gly-Cys-Ser-Gly-Thr-Cys-His-Arg-Arg-Xaa1-Asp-Gly-Lys-Cys-Arg-Gly-Thr-Cys-Asp-Cys-Ser-Gly-Xaa5-Ser-Xaa5-Cys-Arg-Cys-Gly-Asp-Ala-His-His-Phe-Xaa5-Arg-Gly-Cys-Thr-Cys-Thr-Cys-^ (SEQ ID NO:72)

Name: Ca8.3
Species: caracteristicus
Cloned: Yes

DNA Sequence:

ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCATCCTGCCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCGGAAGAGCGGCTTCTA
CGGTACTCTGGCAATGTCTACCAGAGGATGCTCTGGCACTTGCCGTCGTCATCGGGA
CGGCAAGTGTCGGGGTACTTGCGACTGCTCCGGATACAGCTATTGTCGCTGCGGTGA
CGCTCACCATTTTTACCGAGGATGCACGTGTACATGTTAAGGTTGATTAATTCGATC
TTTTAACTCGTTGAACGATTAAAAAAAAAAATTTTAGACGAATATGTTCGAGAAAAA
CCGAAGAC (SEQ ID NO:73)

Translation:

MMSKMGAMFVLLLLFILPSSQQEGDVQARKTHRKSGFYGTLAMSTRGCSGTCRRHRD
GKCRGTCDCSGYSYCRCGDAHHFYRGCTCTC (SEQ ID NO:74)

Toxin Sequence:

Gly-Cys-Ser-Gly-Thr-Cys-Arg-Arg-His-Arg-Asp-Gly-Lys-Cys-Arg-Gly-Thr-Cys-Asp-Cys-Ser-Gly-Xaa5-Ser-Xaa5-Cys-Arg-Cys-Gly-Asp-Ala-His-His-Phe-Xaa5-Arg-Gly-Cys-Thr-Cys-Thr-Cys-^ (SEQ ID NO:75)

Name: Ca8.4
Species: caracteristicus
Cloned: Yes

DNA Sequence:

ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCATCCTGCCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCTGAAGAGAGGCTTCTA
CGGTACTCTGGCAATGTCTACCAGAGGATGCTCTGGCACTTGCCGTCGTCATCGGGA
CGGCAAGTGTCGGGGTACTTGCGACTGCTCCGGATACAGCTATTGTCGCTGCGGTGA
CGCTCACCATTTTTACCGAGGATGCACGTGTACATGTTAAGGTTGATTAATTGACTC
TTTTAACTCGTTGAACGATTAAAAAAAAAAATTTTAGAGCAATATGTTCGAGAAAA
ACCGAAGAC (SEQ ID NO:76)

Translation:

MMSKMGAMFVLLLLFILPSSQQEGDVQARKTHLKRGFYGTLAMSTRGCSGTCRRHRD GKCRGTCDCSGYSYCRCGDAHHFYRGCTCTC (SEQ ID NO:77)

Toxin Sequence:

Gly-Cys-Ser-Gly-Thr-Cys-Arg-Arg-His-Arg-Asp-Gly-Lys-Cys-Arg-Gly-Thr-Cys-Asp-Cys-Ser-Gly-Xaa5-Ser-Xaa5-Cys-Arg-Cys-Gly-Asp-Ala-His-His-Phe-Xaa5-Arg-Gly-Cys-Thr-Cys-Thr-Cys-^ (SEQ ID NO:78)

Name: Ca8.5
Species: caracteristicus
Cloned: Yes

DNA Sequence:

ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGTTTCTTTTCACCCTGCCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCTGAAGAGAGGCTTCTA
CGGTACTCTGGCAATGTCTTCCAGAGGATGCTCTGGCACTTGCCATCGTCGTGAGGA
CGGCAAGTGTCGGGGTACTTGCGACTGCTCCGGATACAGCTATTGTCGCTGCGGTGA
CGCTCACCATTTTTACCGAGGATGTACGTGTACATGTTAAGGTTGATTAATTGACTC
TTTTAACTCGTTGAACGATTAAAAAAAAATTTAGAGCAATATGTTCGAGAAAACCG
AAGAC (SEQ ID NO:79)

Translation:

MMSKMGAMFVLLFLFTLPSSQQEGDVQARKTHLKRGFYGTLAMSSRGCSGTCHRRED GKCRGTCDCSGYSYCRCGDAHHFYRGCTCTC (SEQ ID NO:80)

Toxin Sequence:

Gly-Cys-Ser-Gly-Thr-Cys-His-Arg-Arg-Xaa1-Asp-Gly-Lys-Cys-Arg-Gly-Thr-Cys-Asp-Cys-Ser-Gly-Xaa5-Ser-Xaa5-Cys-Arg-Cys-Gly-Asp-Ala-His-His-Phe-Xaa5-Arg-Gly-Cys-Thr-Cys-Thr-Cys-^ (SEQ ID NO:81)

Name: Ca8.6
Species: caracteristicus
Cloned: Yes

DNA Sequence:

ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCATCCTGCCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCTGAAGAGCGGCTTCTA
CGGTACTCTGGCAATGTCTGCCAGAGGATGCTCTGGCACTTGCCATCGTCGTCAAAA
CGGCGAGTGTCAGGGTACTTGCGACTGCGACGGACACGACCATTGTGACTGCGGTG
ACACTCTCGGTACTTACTCAGGATGCGTGTGTATATGTTAAGGTTGATTAATTGACT
CTTTTAACTCGTTGAACGATTAAAAAAATTTAGAGCAATATGTTCGAGAAAAACCG
AAGAC (SEQ ID NO:82)

Translation:

MMSKMGAMFVLLLLFILPSSQQEGDVQARKTHLKSGFYGTLAMSARGCSGTCHRRQN GECQGTCDCDGHDHCDCGDTLGTYSGCVCIC (SEQ ID NO:83)

Toxin Sequence:

Gly-Cys-Ser-Gly-Thr-Cys-His-Arg-Arg-Gln-Asn-Gly-Xaa1-Cys-Gln-Gly-Thr-Cys-Asp-Cys-Asp-Gly-His-Asp-His-Cys-Asp-Cys-Gly-Asp-Thr-Leu-Gly-Thr-Xaa5-Ser-Gly-Cys-Val-Cys-Ile-Cys-^ (SEQ ID NO:84)

Name: Ca9.1
Species: caracteristicus
Cloned: Yes

DNA Sequence:

GTTACAATGCATCTGTCACTGGCACGCTCAGCTGTCTTGATGTTGCTTCTGCTGTTTG
CCTTGGACAACTTCGTTGGGGTCCAGCCAGGACAGATAACAAGAGATGTGGACAAC
CGCCGTAACCGGCAATCGCGATGGAAGCCAAGGAGTCTCTTCAAGTCACTTCATAA
ACGAGCATCGTGTGGAGGGACTTGCACGGAAAGTGCCGATTGCCCTTCCACGTGTA
GTACTTGCTTACATGCTCAATGCGAGTCAACATGATGTCGCACTACAGCTCTTCTCT
ACAGTGTGTACATCGACCGTACGACGCATCTTTTATTTCTTTGGCTGTTTCATTCGTT
TTCTTGTGTTCATAACATGCGGAGCCCTTCCGTTACCTCTACTGCTCTACACTTAACC
TGATAACCAGAAAATCCAGTACT (SEQ ID NO:85)

Translation:

MHLSLARSAVLMLLLLFALDNFVGVQPGQITRDVDNRRNRQSRWKPRSLFKSLHKRAS CGGTCTESADCPSTCSTCLHAQCEST (SEQ ID NO:86)

Toxin Sequence:

Ala-Ser-Cys-Gly-Gly-Thr-Cys-Thr-Xaa1-Ser-Ala-Asp-Cys-Xaa3-Ser-Thr-Cys-Ser-Thr-Cys-Leu-His-Ala-Gln-Cys-Xaa1-Ser-Thr-^ (SEQ ID NO:87)

Name: Ca9.2
Species: caracteristicus
Cloned: Yes

DNA Sequence:

GTTACAATGCATCTGTCACTGGCACGCTCAGCTGTTTTGATGTTGCTTCTGCTGTTTG
CCTTGGACAACTTCGTTGGGGTCCAACCAGGACAGATAACTAGAGATGTGGACAAC
CGCCGTAACCTGCAATCGCGATGGAAGCCAAGGAGTCTCTTCAAGTCACTTCATAA
ACGAGCATCGTGTGGAGGGACTTGCACGGAAAGTGCCGATTGCCCTTCCACGTGTA
GTACTTGCTTACATGCTCAATGCGAGTGAACATGATGTCGCACTACAGCTCTTCTCT
ACAGTGTGTACATCGACCGACCGTACGACGCATCTTTTATTTCTTTGTCTGTTTCATT
CGTTTTCTTGAGTTCATAACATGCGGAGCCCTTCCGTTACCTCTACTGCTCTACACTT
AAGCTGATAACCAGAAAATCCAGTACT (SEQ ID NO:88)

Translation:

MHLSLARSAVLMLLLLFALDNFVGVQPGQITRDVDNRRNLQSRWKPRSLFKSLHKRAS
CGGTCTESADCPSTCSTCLHAQCE (SEQ ID NO:89)

Toxin Sequence:
Ser-Cys-Gly-Gly-Thr-Cys-Thr-Xaa1-Ser-Ala-Asp-Cys-Xaa3-Ser-Thr-Cys-Ser-Thr-Cys-Leu-His-Ala-Gln-Cys-Xaa1-^ (SEQ ID NO:90)

Name: Cr10.2
Species: circumcisus
Cloned: Yes

DNA Sequence:
tgtgtgtgtgtggttctgggtccaGCATTTGATGGCAGGAATGCCGCAGTCAACGAGAGAGCGCCT
TGGACGGTCGTTTTGTCCACCACGAATTGCTGCGGTTATAATACGATGGAATTCTGC
CCTGCTTGCATGTGCACTTATTCCTGTCCAAAAAAGAAAAAACCAGGAAAAGGCCG
CAGAAACAACTGATGCTCCAGGACCCTCTGAACCACGACGT (SEQ ID NO:91)

Translation:
FDGRNAAVNERAPWTVVLSTTNCCGYNTMEFCPACMCTYSCPKKKKPGKGRRNN
(SEQ ID NO:92)

Toxin Sequence:
Ala-Xaa3-Xaa4-Thr-Val-Val-Leu-Ser-Thr-Thr-Asn-Cys-Cys-Gly-Xaa5-Asn-Thr-Met-Xaa1-Phe-Cys-Xaa3-Ala-Cys-Met-Cys-Thr-Xaa5-Ser-Cys-Xaa3-Lys-Lys-Lys-Lys-Xaa3-Gly-Lys-Gly-Arg-Arg-Asn-Asn-^ (SEQ ID NO:93)

Name: Cn9.1
Species: consors
Cloned: Yes

DNA Sequence:

Translation:
GIFVGVQPEQITRDVDKGYSTDDGHDLLSLLKQISLRACTGSCNSDSECYNFCDCIGTRC
EAQK (SEQ ID NO:94)

Toxin Sequence:
Ala-Cys-Thr-Gly-Ser-Cys-Asn-Ser-Asp-Ser-Xaa1-Cys-Xaa5-Asn-Phe-Cys-Asp-Cys-Ile-Gly-Thr-Arg-Cys-Xaa1-Ala-Gln-Lys-^ (SEQ ID NO:95)

Name: De6.1
Species: delessertii
Isolated: Yes

Toxin Sequence:
Ala-Cys-Lys-Xaa3-Lys-Asn-Asn-Leu-Cys-Ala-Ile-Thr-Xaa1-Met-Ala-Xaa1-Cys-Cys-Ser-Gly-Phe-Cys-Leu-Ile-Xaa5-Arg-Cys-^ (SEQ ID NO:96)

Name: Bromosleeper-Di1
Species: distans
Cloned: Yes

DNA Sequence:
GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCTT
CTACTTCTTGTGCCCATGGCAACCAGTCAACAGGATGGAGGAGAGAAGCAGGCGAT
GCAAAGGGACGCAATCAACGTCGCACCAGGAACATCAATCACTCGGAGAAATGTA
GATCAGGAGTGCATTGACGCCTGTCAGCTGGAGGACAAGAATTGCTGTGGCAGAAC
AGATGGAGAACCCAGATGTGCGAAAATCTGCCTCGGATAATTTCTGTACGCTGTCTC
ATTCATTATTTCATCCGTACGAGTGTAAACGAGACCTATTAGAAAGTCGAAGGTTGT
GCGTAATTTGATAAGCATTGTTTGCTGGGACGAACGGA (SEQ ID NO:97)

Translation:
MSGLGIMVLTLLLLVPMATSQQDGGEKQAMQRDAINVAPGTSITRRNVDQECIDACQL
EDKNCCGRTDGEPRCAKICLG (SEQ ID NO:98)

Toxin Sequence:
Asn-Val-Asp-Gln-Xaa1-Cys-Ile-Asp-Ala-Cys-Gln-Leu-Xaa1-Asp-Lys-Asn-Cys-Cys-Gly-Arg-Thr-Asp-Gly-Xaa1-Xaa3-Arg-Cys-Ala-Lys-Ile-Cys-Leu-# (SEQ ID NO:99)

Name: Bromosleeper-Di2
Species: distans
Cloned: Yes

DNA Sequence:
GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCTT
CTACTTCTTGTGCCCATGGCAACCAGTCAACAGGATGGAGGAGAGAAGCAGGCGAT
GCAAAGGGACGCAATCAACGTCGCACCAGGAACATCAATCACTCGGACAGAAACA
GATCAGGAGTGCATTGACATCTGTAAGCAGGAGGACAAGAAATGCTGCGGCAGATC
AAATGGAGAACCCACATGTGCGAAAATCTGCCTCGGATAATTTCTGTACGCTGTCTC
GTTCATTATTTCGTCAGTACGAGTTTAAACGAGACCTATTAGAAAGTCGAAGGTTCG
TGCTTAATTTGATAAGCATTGTTTGCTGGGATGAACGGA (SEQ ID NO:100)

Translation:
MSGLGIMVLTLLLLVPMATSQQDGGEKQAMQRDAINVAPGTSITRTETDQECIDICKQE
DKKCCGRSNGEPTCAKICLG (SEQ ID NO:101)

Toxin Sequence:
Xaa1-Thr-Asp-Gln-Xaa1-Cys-Ile-Asp-Ile-Cys-Lys-Gln-Xaa1-Asp-Lys-Lys-Cys-Cys-Gly-Arg-Ser-Asn-Gly-Xaa1-Xaa3-Thr-Cys-Ala-Lys-Ile-Cys-Leu-# (SEQ ID NO:102)

Name: Bromosleeper-Di3
Species: distans
Cloned: Yes

DNA Sequence:
GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCTT
CTACTTCTTGTGCCCATGGCAACCAGTCAACAGGATGGAGGAGAGAAGCAGGCGAT
GCAAAGGGACGCAATCAACGTCGCACCAGGAACATCAATCACTCGGAGAGAAACA
GATCAGGAGTGCATTGACACCTGTGAGCAGGAGGACAAGAAATGCTGCGGCAGAA
CAAATGGAGAACCCGTATGTGCGAAAATCTGCTTCGGATAATTTCTGTACGCTGTCT
CATTCATAATTTCATCAGTACGAGTTTAAACGAGACCTATTAGAAAGTCGAAGGTTC
GTGCTTAATTTGATAAGCATTGTTTGCTGGGATGAACGGA (SEQ ID NO:103)

Translation:
MSGLGIMVLTLLLLVPMATSQQDGGEKQAMQRDAINVAPGTSITRRETDQECIDTCEQE
DKKCCGRTNGEPVCAKICFG (SEQ ID NO:104)

Toxin Sequence:

Xaa1-Thr-Asp-Gln-Xaa1-Cys-Ile-Asp-Thr-Cys-Xaa1-Gln-Xaa1-Asp-Lys-Lys-Cys-Cys-Gly-
Arg-Thr-Asn-Gly-Xaa1-Xaa3-Val-Cys-Ala-Lys-Ile-Cys-Phe-# (SEQ ID NO:105)

Name: αA-EIVB
Species: ermineus
Isolated: Yes
Cloned: Yes

DNA Sequence:
ATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCACTTCAG
ATCGTGCATCGGATGACAGGAATACCAACGACAAAGCATCTCGCCTGCTCTCTCAC
GTTGTCAGGGGATGCTGTGGTAAGTATCCCAATGCTGCCTGTCATCCTTGCGGTTGT
ACAGTGGGTAGGCCACCGTATTGTGACAGACCCAGTGGTGGAGGACGCTGATGCTC
CAGGACCCTCTGAACCACGACGT (SEQ ID NO:106)

Translation:
MFTVFLLVVLATTVVSFTSDRASDDRNTNDKASRLLSHVVRGCCGKYPNAACHPCGCT
VGRPPYCDRPSGGGR (SEQ ID NO:107)

Toxin Sequence:
Gly-Cys-Cys-Gly-Lys-Xaa5-Xaa3-Asn-Ala-Ala-Cys-His-Xaa3-Cys-Gly-Cys-Thr-Val-Gly-Arg-
Xaa3-Xaa3-Xaa5-Cys-Asp-Arg-Xaa3-Ser-Gly-Gly-# (SEQ ID NO:108)

Name: Ge3.1
Species: generalis
Cloned: Yes

DNA Sequence:
GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGGTTCTGTTTCCCC
TTACTGCTCTTCCACTGGATGGAGAACAACCTGTAGACCGACATGCCGAGCATATGC
AGGATGACAATTCAGCTGCACAGAACCCCTGGGTTATTGCCATCAGACAGTGTTGC
ACGTTCTGCAACTTTGGATGCCAGCCTTGTTGCGTCCCCTGATAACGTGTTGATGAC
CAACTTTCTCGAG (SEQ ID NO:109)

Translation:
GSMMSKLGVLLTICLVLFPLTALPLDGEQPVDRHAEHMQDDNSAAQNPWVIAIRQCCT
FCNFGCQPCCVP (SEQ ID NO:110)

Toxin Sequence:
Xaa2-Cys-Cys-Thr-Phe-Cys-Asn-Phe-Gly-Cys-Gln-Xaa3-Cys-Cys-Val-Xaa3-^ (SEQ ID NO:111)

Name: C. geographus GS-A
Species: geographus
Cloned: Yes

DNA Sequence:
GCAAGATCATCAGCAGAATGAACCTGACGTGCGTGTTGATCATCGCCGTGCTGTTTC
TGACGGCCTGCCAGCTCATTGCAGCTGATGACTCCAGAGATAACCAGAAGCACCGT
GCAGTGAGGATGAGAGACGCATTGAAGAATTTCAAAGATTCCAGGGCGTGCTCCGG
TAGAGGTTCTAGATGTCCTCCCCAATGCTGCATGGGTTTGACGTGCGGTCGTGAGTA
TCCACCCAGATGCGGTTGATATACGGTGAACAACTGATATTTCCCCTCTGTGCTCTA
CCCTCTTTTGCCTGATTCACCCACACCTATGTGTGGTCATGAACCACTCAGTACCTA
CACCTCTGGTGGCTTCAGAGGACGTATATTAAAATAAAACCACATTGCAATGAAAA
AAAAAAAA (SEQ ID NO:112)

Translation:
MNLTCVLIIAVLFLTACQLIAADDSRDNQKHRAVRMRDALKNFKDSRACSGRGSRCPP
QCCMGLTCGREYPPRCG (SEQ ID NO:113)

Toxin Sequence:
Ala-Cys-Ser-Gly-Arg-Gly-Ser-Arg-Cys-Xaa3-Xaa3-Gln-Cys-Cys-Met-Gly-Leu-Thr-Cys-Gly-Arg-Xaa1-Xaa5-Xaa3-Xaa3-Arg-Cys-# (SEQ ID NO:114)

Name: Conopressin-G
Species: geographus
Isolated: Yes

Toxin Sequence:
Cys-Phe-Ile-Arg-Asn-Cys-Xaa3-Lys-Gly-# (SEQ ID NO:115)

Name: EST66
Species: geographus
Cloned: Yes

DNA Sequence:
TGCTGCCCGAGTAGCAAAGAGGATTCCCTGAACTGCATTGAGACCATGGCGACCAC
GGCCACGTGCATGAAGTCCAACAAGGGGGAGATCTACTCCTATGCGTGCGGCTACT
GCGGCAAGAAGAAGGAGAGCTGTTTCGGCGACAAAAAGCCAGTGACTGACTACCA
GTGCCAGACGCGGAACATTCCCAACCCCTGCGGCGGCGCTGCTCTCTGAAGGCACC
AACAGCACCAACAGCACGATCTCCTGTGTTTCGTCACTGCATTTATGACGTCAAAAC
CACGTCATGCATGATGACGACGATCTCGGCTATGGCATGTATTGAAGAATGGAAAT
AAACCTAGTTTTCAGCTGAAAAAA (SEQ ID NO:116)

Translation:
CCPSSKEDSLNCIETMATTATCMKSNKGEIYSYACGYCGKKKESCFGDKKPVTDYQCQ
TRNIPNPCGGAAL (SEQ ID NO:117)

Toxin Sequence:
Cys-Cys-Xaa3-Ser-Ser-Lys-Xaa1-Asp-Ser-Leu-Asn-Cys-Ile-Xaa1-Thr-Met-Ala-Thr-Thr-Ala-Thr-Cys-Met-Lys-Ser-Asn-Lys-Gly-Xaa1-Ile-Xaa5-Ser-Xaa5-Ala-Cys-Gly-Xaa5-Cys-Gly-Lys-Lys-Lys-Xaa1-Ser-Cys-Phe-Gly-Asp-Lys-Lys-Xaa3-Val-Thr-Asp-Xaa5-Gln-Cys-Gln-Thr-Arg-Asn-Ile-Xaa3-Asn-Xaa3-Cys-Gly-Gly-Ala-Ala-Leu-^ (SEQ ID NO:118)

Name: EST87
Species: geographus
Cloned: Yes

DNA Sequence:
CGGGCGCTGCATTCCGGACGTGAAACAGCATCGCCAGCAAGTGGGCATAGTGCAAG
ACACtCAGAACAAtGACGCACAtAGTCTGANAAAATAACCATGGGTATGCGGATGAN
GTTTAGTGTGTTTCNGCAGGTTGTCNTGGGNACCACTGTCGTTTCCTTCACNTCACGT
CGTGGTCCAAAATCTCGTCGCGGGGAACCTATTCCGACCACTGTAATCAACTACGG
GGAGTGCTGTAAGGATCCATCCTGTTGGGTTAAGGTGAAGGATTTCCAGTGTCCTGG
AGCAAGTCCTCCCAACTGAACCACGACATGTCGCCCTCTGCCTGACCTGCTTCACGT
TCCGTCTCTTTCTGCCACTAGAACTCAACAACTCGATCCAACAGACTCCTACTTTAC
CTCCGTATTCTGAAACTACTTGGATTTGATTGTCTTTAATATCTACTCACACTTGCTG
TTATTACATCATCCAAAATTTAACAAGAACATGAAAGGTGTCTGTTCAAACAAAATC
AGGCAATGACAANGGGGGAAAGTCTCCANTCTATCTGAAAACTGTCACCTGTCACT
CTCTTAACCAGGTTTANAACTGANTACCACTANAGCTGTTGTNCCACATCANGATCA
GNCCAATTTGTANNGTTTCCTTTGCAAAACTTTTGCCTGAAATTCTTGAAAAGAAAC
GCTCACAATGTTGGGAAGTGCTTTTNATTANCTGACAANNTGNCANCATGTTCCNTT
TCANTAANTCTNAAATGNAAACCTCTGTT (SEQ ID NO:119)

Translation:
MGMRMMFSVFLQVVLGTTVVSFTSRRGPKSRRGEPIPTTVINYGECCKDPSCWVKVKD FQCPGASPPN (SEQ ID NO:120)

Toxin Sequence:
Gly-Xaa1-Xaa3-Ile-Xaa3-Thr-Thr-Val-Ile-Asn-Xaa5-Gly-Xaa1-Cys-Cys-Lys-Asp-Xaa3-Ser-Cys-Xaa4-Val-Lys-Val-Lys-Asp-Phe-Gln-Cys-Xaa3-Gly-Ala-Ser-Xaa3-Xaa3-Asn-^ (SEQ ID NO:121)

Name: G12.1
Species: geographus
Cloned: Yes

DNA Sequence:
AGCCTTGATACAGAGCTGGTATCTGCTGTTAATACTTGAAAGAACAAGTGCTGTGA
GCCTTCATCTCTCTCTGACTTTAGTTTGGGTCCTGGAGAAAACCTTGACGGGCAGTA
TGAAAATTTACCTGTGTCTTGCTTTTGTTCTGCTCCTGGCTTCTACCATAGTTGATTC
AGGGCTTCTTGATAAAATTGAGACTATAAGAAACTGGAAACGCGATGACAGCTATT
GTGATGGATGCCTATGCACCATATTAAAAAAAGAGACTTGCACATCGACTATGAGC
TGCAGGGGAACATGCCGAAAAGAGTGGCCATGTTGGGAAGAAGACTGCTACTGTAC
TGAAATCCAAGGTGGAGCTTGCGTCACACCCTCAGAATGCAAACCTGGAGAGTGTT
GAGGATTGGAGTGGCCAGTTCCAGCACATACAGCACCATGGTGCCCTGGACAATCG
TCTATTGAATTGAATATGCCTGTGGCAGGAATCTGTCCTACAAAATAAAAAAATCAT
AAGTTAAAAAA (SEQ ID NO:122)

Translation:
MKIYLCLAFVLLLASTIVDSGLLDKIETIRNWKRDDSYCDGCLCTILKKETCTSTMSCRG
TCRKEWPCWEEDCYCTEIQGGACVTPSECKPGEC (SEQ ID NO:123)

Toxin Sequence:
Asp-Asp-Ser-Xaa5-Cys-Asp-Gly-Cys-Leu-Cys-Thr-Ile-Leu-Lys-Lys-Xaa1-Thr-Cys-Thr-Ser-Thr-Met-Ser-Cys-Arg-Gly-Thr-Cys-Arg-Lys-Xaa1-Xaa4-Xaa3-Cys-Xaa4-Xaa1-Xaa1-Asp-Cys-Xaa5-Cys-Thr-Xaa1-Ile-Gln-Gly-Gly-Ala-Cys-Val-Thr-Xaa3-Ser-Xaa1-Cys-Lys-Xaa3-Gly-Xaa1-Cys-^ (SEQ ID NO:124)

Name: G12.2
Species: geographus
Cloned: Yes

DNA Sequence:
AACGTTGACGGGCAGTATGAACATTTACCTGTGTCTTGCTTTTCTTCTGTTCCTGCCT
TCTACCATAGTTGATTCAGGGCTTCTTGATAAAATTGAGACAATAAGGAATTGGAGA
CGTGATGAAAGCAAGTGTGATCGATGCAATTGCGCCGAATTAAGATCATCCAGATG
CACACAAGCTATCTTCTGCCTTACACCGGAGTTATGCACACCGAGCATCTCATGTCC

GACAGGTGAATGCCGCTGTACTAAGTTCCATCAGTCAAGATGCACTAGATTCGTAG
AATGCGTACCTAATAAGTGTAGAGACGCATAGAGGCCAGTTCCAGCACATACAGCA
CCATGATGCCCTGGACAATCGTGTTGTTGGATTGAATATGCCCGTGGCAGGAATCTG
TCCTACAAAAAA (SEQ ID NO:125)

Translation:
MNIYLCLAFLLFLPSTIVDSGLLDKIETIRNWRRDESKCDRCNCAELRSSRCTQAIFCLTP
ELCTPSISCPTGECRCTKFHQSRCTRFVECVPNKCRDA (SEQ ID NO:126)

Toxin Sequence:
Asp-Xaa1-Ser-Lys-Cys-Asp-Arg-Cys-Asn-Cys-Ala-Xaa1-Leu-Arg-Ser-Ser-Arg-Cys-Thr-Gln-Ala-Ile-Phe-Cys-Leu-Thr-Xaa3-Xaa1-Leu-Cys-Thr-Xaa3-Ser-Ile-Ser-Cys-Xaa3-Thr-Gly-Xaa1-Cys-Arg-Cys-Thr-Lys-Phe-His-Gln-Ser-Arg-Cys-Thr-Arg-Phe-Val-Xaa1-Cys-Val-Xaa3-Asn-Lys-Cys-Arg-Asp-Ala-^ (SEQ ID NO:127)

Name: Scratching,convulsion
Species: geographus
Isolated: Yes

Toxin Sequence:
Lys-Phe-Leu-Ser-Gly-Gly-Phe-Lys-Xaa1-Ile-Val-Cys-His-Arg-Xaa5-Cys-Ala-Lys-Gly-Ile-Ala-Lys-Xaa1-Phe-Cys-Asn-Cys-Xaa3-Asp-# (SEQ ID NO:128)

Name: Contryphan-Im
Species: imperialis
Isolated: Yes

Toxin Sequence:
Xaa2-Cys-Gly-Gln-Ala-Xaa4-Cys-# (SEQ ID NO:129)

Name: Im9.1
Species: imperialis
Cloned: Yes

DNA Sequence:
GTTAAAATGCATCTGTCACTGGCAAGCTCAGCTGCTTTGATGTTGCTTCTGCTTTTTG
CCTTGGGCAACTTCGTTGGGGTCCAGCCAGGACAAATAAGAGATCTGAACAAAGGA
CAGCTCAAGGACAACCGCCGTAACCTGCAATCGCAGAGGAAACAAATGAGTCTCCT
CAAGTCACTTCATGATCGAAATGGGTGTAACGGCAACACGTGTTCCAATAGCCCCT
GCCCTAACAACTGTTATTGCGATACTGAGGACGACTGCCACCCTGACAGGCGTGAA
CATTAGAGATTAGAGAGTTTCCTTGTCAACATGATGTCGCACCACACCTCTGCTCTG
CAGTGTGTACATCGACCAGTCGACGCATCTGTTATTTCTTTGTCTGTTGGATTGTACA
TCGACCAGTCCACGCATCTGTTATTTCTTTGTCTGTTTGATTTGTTTTCGTGTGTTCAT

AACACACAGAGCCTTTCTATTATCTGTATTGCAATACACTTTGCCTGATAACCAGAA
AGTCCAGTGCT (SEQ ID NO:130)

Translation:
MHLSLASSAALMLLLLFALGNFVGVQPGQIRDLNKGQLKDNRRNLQSQRKQMSLLKSL
HDRNGCNGNTCSNSPCPNNCYCDTEDDCHPDRREH (SEQ ID NO:131)

Toxin Sequence:
Asn-Gly-Cys-Asn-Gly-Asn-Thr-Cys-Ser-Asn-Ser-Xaa3-Cys-Xaa3-Asn-Asn-Cys-Xaa5-Cys-
Asp-Thr-Xaa1-Asp-Asp-Cys-His-Xaa3-Asp-Arg-Arg-Xaa1-His-^ (SEQ ID NO:132)

Name: La8.1
Species: laterculatus
Cloned: Yes

DNA Sequence:
ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCACCCTGGCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAACACACCCGAAGAGAGAGTTCCA
TCGTATTCTGCTAAGGCCTGACAGACAGTCCGAAACGGCTTGTAGGTCGCTCGGAA
GCTACCAATGTATGGGTAAATGCCAACTCGGGGTTCATTCCTGGTGTGAATGCATTT
ATAACCGAGGTAGTCAGAAGTCTGGATGCGCGTGTAGGTGTCAAAAGTGATTAATT
GACTCATTTAACTCGTTGAACGATTTAAAAAATCCAGAGCAATATGTTCGAGAAAA
ACCGAAGACGAC (SEQ ID NO:133)

Translation:
MMSKMGAMFVLLLLFTLASSQQEGDVQARKTHPKREFHRILLRPDRQSETACRSLGSY
QCMGKCQLGVHSWCECIYNRGSQKSGCACRCQK (SEQ ID NO:134)

Toxin Sequence:
Xaa2-Ser-Xaa1-Thr-Ala-Cys-Arg-Ser-Leu-Gly-Ser-Xaa5-Gln-Cys-Met-Gly-Lys-Cys-Gln-Leu-
Gly-Val-His-Ser-Xaa4-Cys-Xaa1-Cys-Ile-Xaa5-Asn-Arg-Gly-Ser-Gln-Lys-Ser-Gly-Cys-Ala-
Cys-Arg-Cys-Gln-Lys-^ (SEQ ID NO:135)

Name: Lv6.2
Species: lividus
Cloned: Yes

DNA Sequence:
GGATCCATGAAACTGACGTGTGTGGTGATCATCGCCGTGCTGTTCCTGACGGCCAGT
CAGCTCATTACAGCTGATTACTCCAGAGATAAGCAGGAGTATCGTGCAGAGAGGCT
GAGAGACGCAATGGGGAAATTCAAAGGTTCCAGGTCGTGCGGACATAGTGGTGCAG
GTTGTTATACTCGCCCTTGCTGCCCTGGTCTGCATTGCTCTGGCGGCCAAGCTGGAG
GCCTGTGCGTGTAATAGTAATAATCTGGCGTCTGATATTTCCAGTCTGTGCTCTACC
CTCTTTTGCCTGAGTCATCCATACCTGTGCTCGAG (SEQ ID NO:136)

Translation:
MKLTCVVIIAVLFLTASQLITADYSRDKQEYRAERLRDAMGKFKGSRSCGHSGAGCYT
RPCCPGLHCSGGQAGGLCV (SEQ ID NO:137)

Toxin Sequence:
Ser-Cys-Gly-His-Ser-Gly-Ala-Gly-Cys-Xaa5-Thr-Arg-Xaa3-Cys-Cys-Xaa3-Gly-Leu-His-Cys-Ser-Gly-Gly-Gln-Ala-Gly-Gly-Leu-Cys-Val-^ (SEQ ID NO:138)

Name: Lv6.3
Species: lividus
Cloned: Yes

DNA Sequence:
GGATCCATGAAACTGACGTGTGTGGTGATCATATCCGTGCTGTTCCTGACGGCCAGT
GAGTTCCTTACAGCTGATTACTCCAGAGATAAGCGGCAGTACCGTGCTGTGAGGTTG
AGAGACGCAATGCGGAATTTCAAAGGTACCAGGGACTGCGGGGAATCAGGTCAAG
GTTGCTATAGTGTACGTCCTTGCTGCCCTGGTCTGATTTGCAAAGGCACCGGTGGTG
GAGGCCTGTGCCGGCCCTCTGGCATCTGATATCTCCCCTCTGTGCTCCACCCTCTTTT
GCCTGAGTCATCCATACCTGTGCTCGAG (SEQ ID NO:139)

Translation:
MKLTCVVIISVLFLTASEFLTADYSRDKRQYRAVRLRDAMRNFKGTRDCGESGQGCYS
VRPCCPGLICKGTGGGGLCRPSGI (SEQ ID NO:140)

Toxin Sequence:
Asp-Cys-Gly-Xaa1-Ser-Gly-Gln-Gly-Cys-Xaa5-Ser-Val-Arg-Xaa3-Cys-Cys-Xaa3-Gly-Leu-Ile-Cys-Lys-Gly-Thr-Gly-Gly-Gly-Gly-Leu-Cys-Arg-Xaa3-Ser-Gly-Ile-^ (SEQ ID NO:141)

Name: Convulsant
Species: magus
Isolated: Yes

Toxin Sequence:
Val-Xaa5-Xaa1-Thr-His-Xaa3-^ (SEQ ID NO:142)

Name: MAG-1
Species: magus
Isolated: Yes

Toxin Sequence:
Arg-Xaa3-Lys-Asn-Ser-Xaa4-^ (SEQ ID NO:143)

Name: MAG-2
Species: magus
Isolated: Yes

Toxin Sequence:
Ala-Arg-Xaa3-Lys-Asn-Ser-Xaa4-? (SEQ ID NO:144)

Name: MAG-3
Species: magus
Isolated: Yes

Toxin Sequence:

Arg-Xaa3-Lys-Asn-Ser-Xaa4-^ (SEQ ID NO:145)

Name: Mi6.2
Species: miles
Cloned: Yes

DNA Sequence:
GGATCCATGAAACTGACGTGCGTGGTGATCGTCGCCGTGCTGTTCCTGACGGCCTGT
CAACTCATTACTGCTGCGAATTACGCCAGAGATGAACAGGAGTACCCCGCTGTGAG
GTCGAGCGACGTGATGCAGGATTCCGAAGACTTGACGTTGACCAAGAAATGCACGG
ACGATTCTCAGTTCTGTAACCCTTCGAATCATGACTGCTGCAGTGGGAAGTGTATCG
ACGAAGGAGACAACGGCATATGCGCTATAGTCCCTGAAAACTCTTAACAATGTATA
CTGACATTTCCCCCTCTGTGCTCCGCCGTCCGTGGCCTGACTCGTCCATCCTTGGGCG
TGGTCATGAACCGCTCGGTT (SEQ ID NO:146)

Translation:
MKLTCVVIVAVLFLTACQLITAANYARDEQEYPAVRSSDVMQDSEDLTLTKKCTDDSQ
FCNPSNHDCCSGKCIDEGDNGICAIVPENS (SEQ ID NO:147)

Toxin Sequence:
Cys-Thr-Asp-Asp-Ser-Gln-Phe-Cys-Asn-Xaa3-Ser-Asn-His-Asp-Cys-Cys-Ser-Gly-Lys-Cys-Ile-Asp-Xaa1-Gly-Asp-Asn-Gly-Ile-Cys-Ala-Ile-Val-Xaa3-Xaa1-Asn-Ser-^ (SEQ ID NO:148)

Name: Mi6.3
Species: miles
Cloned: Yes

DNA Sequence:
GGATCCATGAAACTGACGTGTGTGGTGATCGTCGCCGTGCTGTTCCTGACGGCCTGT
CAACTCATTACTGCTGCGAATTACGCCAGAGATGAACAGGAGTACCCTGCTGTGAG
GTCGAGCGACGTGATGCAGGATTCCGAAGACCTGACGTTGACCAAGAAATGCACGG

AGGATTCTCAGTTCTGTAACCCTTCGAATCATGACTGCTGCAGTGGGAAGTGTATCG
ACGAAGGAGACAACGGCATATGCGCTATAGTCCCTGAAAACTCTTAACAATGTATA
CTGACATTTCCCCCTCTGTGCTCCGCCGTCCGTGGCCTGACTCGTCCATCCTTGGGCG
TGGTCATGAACCGCTCG (SEQ ID NO:149)

Translation:
MKLTCVVIVAVLFLTACQLITAANYARDEQEYPAVRSSDVMQDSEDLTLTKKCTEDSQ
FCNPSNHDCCSGKCIDEGDNGICAIVPENS (SEQ ID NO:150)

Toxin Sequence:
Cys-Thr-Xaa1-Asp-Ser-Gln-Phe-Cys-Asn-Xaa3-Ser-Asn-His-Asp-Cys-Cys-Ser-Gly-Lys-Cys-
Ile-Asp-Xaa1-Gly-Asp-Asn-Gly-Ile-Cys-Ala-Ile-Val-Xaa3-Xaa1-Asn-Ser-^ (SEQ ID NO:151)

Name: Mf6.1
Species: miliaris
Cloned: Yes

DNA Sequence:
GGATCCATGAACTGACGTGTGTGGTGATCATCGCCGTGCTGTTCCTGACGGCCTGTC
AACTCACTACAGCTGTGACTTCCTCCAGAGGTCAACAGAAGCATCGTGCTCTGAGGT
CAACTGACAAAAACTCCAGGATGACCAAGCGTTGCACGCCTCCAGGTGGACTCTGT
TACCATGCTTATCCCTGCTGCAGCAAGACTTGCAATCTCGATACCAGCCAATGTGAG
CCTAGGTGGTCATGAACCACTCAATACCCTCTCCTCTGGAGGCTTCAGAGGAACTAC
ATTGAAATAAAACCGCATTGCAACGAAAAAAAAAAAAAAAAAA (SEQ ID NO:152)

Translation:
LTCVVIIAVLFLTACQLTTAVTSSRGQQKHRALRSTDKNSRMTKRCTPPGGLCYHAYPC
CSKTCNLDTSQCEPRWS (SEQ ID NO:153)

Toxin Sequence:
Cys-Thr-Xaa3-Xaa3-Gly-Gly-Leu-Cys-Xaa5-His-Ala-Xaa5-Xaa3-Cys-Cys-Ser-Lys-Thr-Cys-
Asn-Leu-Asp-Thr-Ser-Gln-Cys-Xaa1-Xaa3-Arg-Xaa4-Ser-^ (SEQ ID NO:154)

Name: Mn10.3
Species: monachus
Cloned: Yes

DNA Sequence:
tgtgtgtgtgtggttctgggtccaGCATCTGATGTCAGGAATGCCGCAGTCCACGAAAGACAGAAG
GATCTGGTCGTTACGGCCACCACGACTTGCTGTGGTTATAATCCGATGACAATGTGC
CCTCCTTGCATGTGCACTAATACCTGCAAAAAAAGTGGCTGATGCTCCAGGACCCTC
TGAACCACGACGT (SEQ ID NO:155)

Translation:
SDVRNAAVHERQKDLVVTATTTCCGYNPMTMCPPCMCTNTCKKSG (SEQ ID NO:156)

Toxin Sequence:
Xaa2-Lys-Asp-Leu-Val-Val-Thr-Ala-Thr-Thr-Thr-Cys-Cys-Gly-Xaa5-Asn-Xaa3-Met-Thr-Met-Cys-Xaa3-Xaa3-Cys-Met-Cys-Thr-Asn-Thr-Cys-Lys-Lys-Ser-# (SEQ ID NO:157)

Name: Mn8.1
Species: monachus
Cloned: Yes

DNA Sequence:
ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCACCCTGGCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAACAAGCCTGAAGAGCGACTTCTA
TCGTGCTCTGAGAGGGTATGACAGACAGTGCACTCTTGTCAACAATTGTGACCGGA
ACGGTGAGCGTGCGTGTAACGGTGATTGCTCTTGCGAGGGCCAGATTTGTAAATGC
GGTTATAGAGTCAGTCCTGGGAAGTCAGGATGCGCGTGTACTTGTAGAAATGCCAA
ATGAATCATTTAACTCGTTGAAAGATTTTTTAAAAATCCAGAGCTATATGTTCGAGA
AAAACCGAAGAC (SEQ ID NO:158)

Translation:
MMSKMGAMFVLLLLFTLASSQQEGDVQARKTSLKSDFYRALRGYDRQCTLVNNCDRN
GERACNGDCSCEGQICKCGYRVSPGKSGCACTCRNAK (SEQ ID NO:159)

Toxin Sequence:
Xaa2-Cys-Thr-Leu-Val-Asn-Asn-Cys-Asp-Arg-Asn-Gly-Xaa1-Arg-Ala-Cys-Asn-Gly-Asp-Cys-Ser-Cys-Xaa1-Gly-Gln-Ile-Cys-Lys-Cys-Gly-Xaa5-Arg-Val-Ser-Xaa3-Gly-Lys-Ser-Gly-Cys-Ala-Cys-Thr-Cys-Arg-Asn-Ala-Lys-^ (SEQ ID NO:160)

Name: Pn1.3
Species: pennaceus
Cloned: Yes

DNA Sequence:
ATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGCTGACTGCATCTGCACCTAGCG
TTGATGCCAAAGTTCATCTGAAGACCAAAGGTGATGGGCCCCTGTCATCTTTCCGAG
ATAATGCAAAGAGTACCCTACAAAGACTTCAGGACAAAAGCACTTGCTGTGGCTTT
AAGATGTGTATTCCTTGTCGTTAACCAGCATGAAGGATCC (SEQ ID NO:161)

Translation:
MRCLPVFVILLLLTASAPSVDAKVHLKTKGDGPLSSFRDNAKSTLQRLQDKSTCCGFKM
CIPCR (SEQ ID NO:162)

Toxin Sequence:
Ser-Thr-Cys-Cys-Gly-Phe-Lys-Met-Cys-Ile-Xaa3-Cys-Arg-^ (SEQ ID NO:163)

Name: Pn9.1
Species: pennaceus
Cloned: Yes

DNA Sequence:
ATGTTGCTTCTGCTGTTTGCCTTGGGCAGCTTCGTTGTGGTCCAGTCAGGACAGATA
ACAAGAGATGTGGACAATGGGCAGCTCGCGGACAACCGCCGTACCCTGCGATCGCA
GTGGAAGCAAGTGAGTTTCTTCAAGTCACTTGATAAACGACTGACTTGTAACGATCC
TTGCCAGATGCATTCCGATTGCGGCATATGTGAATGCGTGGAAAATAAATGCATATT
TTTCATGTAAACGGATTGAGTTTGCTTGTCAACACAATGTCGCACTGCAGCTCTTCT
CTACCGGTGGGTACATCGACCAAACGACGCATCTTTTATTTCTTTGTCTGTTTCGTTT
GTTCTCCTGTGTTCATAACGTACAGAGCCCTTTAACTACCCTTACTGCTCTTCACTTA
ACCTGATAACCTGAAGGTCCGGTGCAGCTGGCGTAGCCTTCACAGTTTCG (SEQ ID NO:164)

Translation:
MLLLLFALGSFVVVQSGQITRDVDNGQLADNRRTLRSQWKQVSFFKSLDKRLTCNDPC
QMHSDCGICECVENKCIFFM (SEQ ID NO:165)

Toxin Sequence:
Leu-Thr-Cys-Asn-Asp-Xaa3-Cys-Gln-Met-His-Ser-Asp-Cys-Gly-Ile-Cys-Xaa1-Cys-Val-Xaa1-Asn-Lys-Cys-Ile-Phe-Phe-Met-^ (SEQ ID NO:166)

Name: Pu6.1
Species: pulicarius
Cloned: Yes

DNA Sequence:
ATGAAACTGACGTGTGTGGTGATCGTCGCCGTGCTGTTCCTGACGGCCTGTCAACTC
AGTACAGCTGATGACTCCAGAGATGAGCAGCAGGATCCTTTGGTGAGGTCGCATCG
TGAGGAGCAGAAAGCCGAGGACCCCAAGACGGCCGAGAGATGTTCAGATTTCGGA
TCCGACTGTGTTCCTGCTACTCATAACTGCTGCAGTGGTGAATGTTTTGGCTTCGAG
GACTTCGGCTTATGCACGTAAAACTGGTCTGACGTCTGATATTCCCCCCTCTGTCCTT
CATCCTCTTTTGCCTGATTCATCCATACCTATATGTGCTCCTGAACCGCTGTGTACCT
TTACCCTGGTGGCTTCAGAGGACGTTATATCAAAATAAAACCGCGTTGCAATGACA
AAAAAAAAAAAAAAAA (SEQ ID NO:167)

Translation:
MKLTCVVIVAVLFLTACQLSTADDSRDEQQDPLVRSHREEQKAEDPKTAERCSDFGSD
CVPATHNCCSGECFGFEDFGLCT (SEQ ID NO:168)

Toxin Sequence:
Cys-Ser-Asp-Phe-Gly-Ser-Asp-Cys-Val-Xaa3-Ala-Thr-His-Asn-Cys-Cys-Ser-Gly-Xaa1-Cys-Phe-Gly-Phe-Xaa1-Asp-Phe-Gly-Leu-Cys-Thr-^ (SEQ ID NO:169)

Name: Bromosleeper-P1
Species: purpurascens
Cloned: Yes

DNA Sequence:
GACAGGATTGAACAAAATTCAGGATGTCAAGATTTGGAATCATGGTGCTAACCTTT
CTACTTCTTGTGTCCATGGCAACCAGCCATCGTTATGCAAGAGGGAAGCAGGCGAC
GCGAAGGAACGCAATCAACATCAGACGGAGAAGCACACCAAAAACTGAGGCGTGC
GAAGAGGTCTGTGAGCTGGAAGAAAAGCACTGCTGCTGCATAAGAAGTGACGGAC
CCAAATGTTCCCGTAAGTGCCTGTTGTCAATCTTCTGTTAGTTTCTGTACACTGTCTC
ATTCATTATCTTATCAGTACAAGTGTAAACGAGACATGTCAGAAAGTCGAAGGTTGT
GCGTAATTTGATAAGTATTGTTTGCTGGGATGAACGGA (SEQ ID NO:170)

Translation:
MSRFGIMVLTFLLLVSMATSHRYARGKQATRRNAINIRRRSTPKTEACEEVCELEEKHC
CCIRSDGPKCSRKCLLSIFC (SEQ ID NO:171)

Toxin Sequence:
Xaa3-Lys-Thr-Xaa1-Ala-Cys-Xaa1-Xaa1-Val-Cys-Xaa1-Leu-Xaa1-Xaa1-Lys-His-Cys-Cys-
Cys-Ile-Arg-Ser-Asp-Gly-Xaa3-Lys-Cys-Ser-Arg-Lys-Cys-Leu-Leu-Ser-Ile-Phe-Cys-^ (SEQ ID
NO:172)

Name: Bromosleeper-P2
Species: purpurascens
Cloned: Yes

DNA Sequence:
GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCTT
CTACTTCTTGTGTCCATGGCAACCAACCATCAGGATAGAGGAGAGAAGCAGGTGAC
GCAAAGGGACGCAATCAACGTCAGACGGAGAAGATCAATCACCCAGCAAGTCGTA
TCTGAGGAGTGCAAAAAGTACTGTAAGAAACAGAACAAGAATTGCTGCAGCAGTAA
ACATGAAGAACCCAGATGTGCCAAGATATGCTTCGGATAGTTTCTGTACACGGTCTC
ATTCATTATTTTATCAGTACAAGTTAAACGAGACCTATCAGAAGTCGAAGGTTGTGC
ATAATTTGATAAACATTGTTTGCTGGGATGAACGGA (SEQ ID NO:173)

Translation:
MSGLGIMVLTLLLLVSMATNHQDRGEKQVTQRDAINVRRRRSITQQVVSEECKKYCKK
QNKNCCSSKHEEPRCAKICFG (SEQ ID NO:174)

Toxin Sequence:
Val-Val-Ser-Xaa1-Xaa1-Cys-Lys-Lys-Xaa5-Cys-Lys-Lys-Gln-Asn-Lys-Asn-Cys-Cys-Ser-Ser-
Lys-His-Xaa1-Xaa1-Xaa3-Arg-Cys-Ala-Lys-Ile-Cys-Phe-# (SEQ ID NO:175)

Name: P29
Species: purpurascens

Isolated: Yes

Toxin Sequence:
Asp-Cys-Cys-Gly-Val-Lys-Leu-Xaa1-Met-Cys-His-Xaa3-Cys-Leu-Cys-Asp-Asn-Ser-Cys-Lys-Asn-Xaa5-Gly-Lys-# (SEQ ID NO:176)

Name: P4.1
Species: purpurascens
Cloned: Yes

DNA Sequence:
ATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCACTTCAG
ATCGTGCATCGGATGACAGGAATACCAACGACAAAGCATCTCGCCTGCTCTCTCAC
GTTGTCAGGGGATGCTGTGGTAGCTATCCCAATGCTGCCTGTCATCCTTGCGGTTGT
AAAGATAGGCCATCGTATTGTGGTCAAGGACGCTGATGCTCCAGGACCCTCTGAAC
CACGACGT (SEQ ID NO:177)

Translation:
MFTVFLLVVLATTVVSFTSDRASDDRNTNDKASRLLSHVVRGCCGSYPNAACHPCGCK
DRPSYCGQGR (SEQ ID NO:178)

Toxin Sequence:
Gly-Cys-Cys-Gly-Ser-Xaa5-Xaa3-Asn-Ala-Ala-Cys-His-Xaa3-Cys-Gly-Cys-Lys-Asp-Arg-Xaa3-Ser-Xaa5-Cys-Gly-Gln-# (SEQ ID NO:179)

Name: P4.2
Species: purpurascens
Cloned: Yes

DNA Sequence:
ATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCACCGTAG
ATCGTGCAACTGATGGCAGGAGTGCTGCAGCCATAGCGTTTGCCCTGATCGCTCCGA
CCGTCCGGGAAGGATGCTGTTCTAATCCTGCCTGTCATCCTTGCGGTTGTAAAGATA
GGCCATCGTATTGTGGTCAAGGACGCTGATGCTCCAGGACCCTCTGAACCACGACG
T (SEQ ID NO:180)

Translation:
MFTVFLLVVLATTVVSFTVDRATDGRSAAAIAFALIAPTVREGCCSNPACHPCGCKDRP
SYCGQGR (SEQ ID NO:181)

Toxin Sequence:
Xaa1-Gly-Cys-Cys-Ser-Asn-Xaa3-Ala-Cys-His-Xaa3-Cys-Gly-Cys-Lys-Asp-Arg-Xaa3-Ser-Xaa5-Cys-Gly-Gln-# (SEQ ID NO:182)

Name: P8.1
Species: purpurascens
Cloned: Yes

DNA Sequence:
ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCACCCTGGCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAACACGCCTGACGAGGGACTTCTA
TCGTACTCTGCCAGTGTCTACTAGAGGATGCAGCGGCTCCCCTTGTTTTAAAAACAA
AACGTGTCGGGATGAATGCATATGCGGCGGCTTATCCAATTGTTGGTGTGGCTACGG
CGGTAGTCGAGGATGCAAGTGTACATGTAGAGAGTGATTAATCGACTCTTTAACTC
GTTGAATTATTTAAAAAATCCAGAGCAATATGTTCGAGAAAAACCGAAGAC (SEQ ID NO:183)

Translation:
MMSKMGAMFVLLLLFTLASSQQEGDVQARKTRLTRDFYRTLPVSTRGCSGSPCFKNKT
CRDECICGGLSNCWCGYGGSRGCKCTCRE (SEQ ID NO:184)

Toxin Sequence:
Gly-Cys-Ser-Gly-Ser-Xaa3-Cys-Phe-Lys-Asn-Lys-Thr-Cys-Arg-Asp-Xaa1-Cys-Ile-Cys-Gly-Gly-Leu-Ser-Asn-Cys-Xaa4-Cys-Gly-Xaa5-Gly-Gly-Ser-Arg-Gly-Cys-Lys-Cys-Thr-Cys-Arg-Xaa1-^ (SEQ ID NO:185)

Name: U021 homolog
Species: purpurascens
Cloned: Yes

DNA Sequence:
CGACCTCAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGA
CCATCTGTCTGCTTCTGTTTCCCATTACTGCTCTTCTGATGGATGGAGATCAACCTGC
AGACCGACCTGCAGAACGTATGGATTACGACATTTCATCTGAGGTGCATCGTTTGCT
TGAAAGGAGACACCCGCCCTGTTGCATGTACGGCAGATGCCGTCGATATCCCGGAT
GCTCTAGTGCCTCTTGTTGCCAGGGAGGATAACGTGTTGATGACCAACTTTGTTACA
CGGCTACGTCAAGTGTCTACTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:186)

Translation:
MMSKLGALLTICLLLFPITALLMDGDQPADRPAERMDYDISSEVHRLLERRHPPCCMYG
RCRRYPGCSSASCCQGG (SEQ ID NO:187)

Toxin Sequence:
His-Xaa3-Xaa3-Cys-Cys-Met-Xaa5-Gly-Arg-Cys-Arg-Arg-Xaa5-Xaa3-Gly-Cys-Ser-Ser-Ala-Ser-Cys-Cys-Gln-Gly-# (SEQ ID NO:188)

Name: ψ-PIIIF
Species: purpurascens

Isolated: Yes

Toxin Sequence:

Gly-Xaa3-Xaa3-Cys-Cys-Leu-Xaa5-Gly-Ser-Cys-Arg-Xaa3-Phe-Xaa3-Gly-Cys-Xaa5-Asn-Ala-Leu-Cys-Cys-Arg-Lys-# (SEQ ID NO:189)

Name: Qc6.4
Species: quercinus
Cloned: Yes

DNA Sequence:

GGATCCATGAAACTGACGTGCGTGGTGATCATCGCCGTGCTGTTTCTGACAGCCAGT
CAGCTCGTTACAGCTGATTACACCAGAGATAAATGGCAATACCCTGCAGCGAGTTT
GAGAGGCGGAATGTGGAATTTGAGAGATACCAGGGCGTGCTCGCAAGTAGGTGAA
GCTTGTTTTCCTCAGAAACCTTGCTGCCCTGGATTCCTTTGCAATCACATCGGAGGC
ATGTGCCACCACTAGTAACAGTCTGGCATCTGATATTTCCCCTCTGCGCTCCACCCT
CTTTTGGCTGATTCATCCTTACCTGTGTGTGGTCATGAACCACTCAGTAGCTACACCT
CTGGTGGCTTCAGAGGACGTATATCAAAATAAAACCACATTGCAAAAAAAAAAAAAA
AAAA (SEQ ID NO:190)

Translation:

MKLTCVVIIAVLFLTASQLVTADYTRDKWQYPAASLRGGMWNLRDTRACSQVGEACF
PQKPCCPGFLCNHIGGMCHH (SEQ ID NO:191)

Toxin Sequence:

Ala-Cys-Ser-Gln-Val-Gly-Xaa1-Ala-Cys-Phe-Xaa3-Gln-Lys-Xaa3-Cys-Cys-Xaa3-Gly-Phe-Leu-Cys-Asn-His-Ile-Gly-Gly-Met-Cys-His-His-^ (SEQ ID NO:192)

Name: QcII
Species: quercinus
Isolated: Yes

Toxin Sequence:

Asp-Cys-Gln-Xaa3-Cys-Gly-His-Asn-Val-Cys-Cys-^ (SEQ ID NO:193)

Name: EST171
Species: radiatus
Cloned: Yes

DNA Sequence:

CATGAACTGTCTCGTACTGGCTTTGGTTACCATCGGTCTTCTGGCTGCAACAACCGC
AGCCCCTCTGGACACCACCACGGTCCTCCTCAGCACAACTACACGCGATGTCAAGG
GCTGTGTGTACGAGGGCATAGAGTACAGTGTCGGAGAGACCTACCAGGCAGACTGC

AACACGTGTCGCTGTGATGGCTTTGACCTGGCTACATGCACCGTCGCGGGCTGCACA
GGCTTTGGACCCGAGTGATTGGTACTATTCCACACCTAGCAATGTTCACACTGGAAC
CGGAACTTGATACTACCTTCTAAATATAATCAATTTGTTTCAAAAGGCCCAAA (SEQ ID NO:194)

Translation:
MNCLVLALVTIGLLAATTAAPLDTTTVLLSTTTRDVKGCVYEGIEYSVGETYQADCNTC
RCDGFDLATCTVAGCTGFGPE (SEQ ID NO:195)

Toxin Sequence:
Gly-Cys-Val-Xaa5-Xaa1-Gly-Ile-Xaa1-Xaa5-Ser-Val-Gly-Xaa1-Thr-Xaa5-Gln-Ala-Asp-Cys-Asn-Thr-Cys-Arg-Cys-Asp-Gly-Phe-Asp-Leu-Ala-Thr-Cys-Thr-Val-Ala-Gly-Cys-Thr-Gly-Phe-Gly-Xaa3-Xaa1-^ (SEQ ID NO:196)

Name: EST202
Species: radiatus
Cloned: Yes

DNA Sequence:
GTGAGAGTCCAACAGCCCAAACCTTTCAACTCACTATGTGGCAGTTGCAGTTTTCAA
CGTCTGGACAGGATTCAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTA
ACCCTTCTACTTCTTGTGTCCATGGCAACCAGTCGTCAGGATAGAGGAGTGGGACAG
CTGATGCCACGCGTCTCGTTCAAAGCCTGCAAATCAAATTATGATTGCCCCCAGCGT
TTCAAATGCTGCAGTTACACCTGGAATGGATCCAGTGGATACTGTAAACGTGTTTGC
TATCTTTATCGTTAGTGTAATACACAAAGTGACTCTGTTCATTCCTCTCCATCATCTC
TTTAGAAACAACACGGTGTCGAGATCGTTTCTTTGTGATGAAGAGTAGTATCACGGG
CAGAGTTCACTAGAGATCTCAAATGAAAAACAAGATTATTTAGTAAGTTGGGGAAA
ATCTGGATCTCGAAAAGATTCCTTGAAAACTCCGTATTTAACACGCTTGAGAGATGA
TAATAAAGAATTCTGAAAGACaAA (SEQ ID NO:197)

Translation:
MSGLGIMVLTLLLLVSMATSRQDRGVGQLMPRVSFKACKSNYDCPQRFKCCSYTWNG
SSGYCKRVCYLYR (SEQ ID NO:198)

Toxin Sequence:
Ala-Cys-Lys-Ser-Asn-Xaa5-Asp-Cys-Xaa3-Gln-Arg-Phe-Lys-Cys-Cys-Ser-Xaa5-Thr-Xaa4-Asn-Gly-Ser-Ser-Gly-Xaa5-Cys-Lys-Arg-Val-Cys-Xaa5-Leu-Xaa5-Arg-^ (SEQ ID NO:199)

Name: R8.1
Species: radiatus
Cloned: Yes

DNA Sequence:
ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCACCCTGGCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAACACACCCGAAGAGAGAGTTCCA

ACGTATTCTGCTAAGGTCTGGCAGAAAGTGCAATTTCGACAAATGTAAAGGTACCG
GAGTCTACAATTGTGGGGAATCCTGCTCATGCGAAGGTTTGCACAGTTGTCGCTGCA
CTTATAACATCGGTTCTATGAAGTCTGGATGCGCGTGTATTTGTACATACTATTAAT
GATTAATTGACTCGTTTAACTCGTTGAACGATTTAAAAAATCCAGAGCAATATGTTC
GAGAAAAACCGAAGAC (SEQ ID NO:200)

Translation:
MMSKMGAMFVLLLLFTLASSQQEGDVQARKTHPKREFQRILLRSGRKCNFDKCKGTG
VYNCGESCSCEGLHSCRCTYNIGSMKSGCACICTYY (SEQ ID NO:201)

Toxin Sequence:
Lys-Cys-Asn-Phe-Asp-Lys-Cys-Lys-Gly-Thr-Gly-Val-Xaa5-Asn-Cys-Gly-Xaa1-Ser-Cys-Ser-Cys-Xaa1-Gly-Leu-His-Ser-Cys-Arg-Cys-Thr-Xaa5-Asn-Ile-Gly-Ser-Met-Lys-Ser-Gly-Cys-Ala-Cys-Ile-Cys-Thr-Xaa5-Xaa5-^ (SEQ ID NO:202)

Name: R8.2
Species: radiatus
Cloned: Yes

DNA Sequence:
ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCACCCTGGCATCCA
GGCAGCAGGAAGGAGATGTCCAGGCAAGGAAAACACGCCTGACGAGCGACTTCTA
TAGTGTTCTGCAAAGGTATGGACTAGGATGCGCTGGCACTTGTGGTTCAAGCAGCA
ATTGTGTTAGAGATTATTGTGACTGCCCAAAACCCAATTGTTACTGCACTGGCAAAG
GCTTTCGTCAACCAGGATGCGGGTGTTCATGTTTGGGGTGATTAATTGGCTCTTTTA
ACTCGTTGAACGATTTAAAAAATCCAGAGCAATATGTTCGAGAAAAACCGAAGAC
(SEQ ID NO:203)

Translation:
MMSKMGAMFVLLLLFTLASRQQEGDVQARKTRLTSDFYSVLQRYGLGCAGTCGSSSN
CVRDYCDCPKPNCYCTGKGFRQPGCGCSCLG (SEQ ID NO:204)

Toxin Sequence:
Xaa5-Gly-Leu-Gly-Cys-Ala-Gly-Thr-Cys-Gly-Ser-Ser-Ser-Asn-Cys-Val-Arg-Asp-Xaa5-Cys-Asp-Cys-Xaa3-Lys-Xaa3-Asn-Cys-Xaa5-Cys-Thr-Gly-Lys-Gly-Phe-Arg-Gln-Xaa3-Gly-Cys-Gly-Cys-Ser-Cys-Leu-# (SEQ ID NO:205)

Name: Bromosleeper-Sn
Species: sponsalis
Cloned: Yes

DNA Sequence:
GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTGACCCTT
TTGCTTCTTGTGTCCATGGCAACCAGCCATAAGGATGGAGGAGAGAAGCAGGCGAT
GCAAAGGGACGCAATCAACGTCAGACTGAGAAGATCACTCACTCGGAGAGCAGTA

ACTGAGGCGTGCACGGAGGACTGTAAGACTCAGGACAAGAAGTGCTGCGGCGAAA
TGAATGGACAACACACATGTGCCAAGATATGCCTCGGATAGTCTCTGTACGCTGTCT
CATTCATTATCTCATCAGTACAAGTGTAAACGAGACAGGTCAGAAAGTCGAAGGTT
GTTCGAAATTTGATAAGCATTGTTTACTGGGACGAACGGA (SEQ ID NO:206)

Translation:
MSGLGIMVLTLLLLVSMATSHKDGGEKQAMQRDAINVRLRRSLTRRAVTEACTEDCKT
QDKKCCGEMNGQHTCAKICLG (SEQ ID NO:207)

Toxin Sequence:

Ala-Val-Thr-Xaa1-Ala-Cys-Thr-Xaa1-Asp-Cys-Lys-Thr-Gln-Asp-Lys-Lys-Cys-Cys-Gly-Xaa1-Met-Asn-Gly-Gln-His-Thr-Cys-Ala-Lys-Ile-Cys-Leu-# (SEQ ID NO:208)

Name: Contryphan-Sm-dW4, V7
Species: stercusmuscarum
Isolated: Yes

Toxin Sequence:
Gly-Cys-Xaa3-Xaa4-Gln-Xaa3-Val-Cys-# (SEQ ID NO:209)

Name: Conopressin-S
Species: striatus
Isolated: Yes

Toxin Sequence:
Cys-Ile-Ile-Arg-Asn-Cys-Xaa3-Arg-Gly-# (SEQ ID NO:210)

Name: S6.4
Species: striatus
Cloned: Yes

DNA Sequence:
AGGTCGACTCGCTGCTTGCCTGACGGAACGTCTTGCCTTTTTAGTAGGATCAGATGC
TGCGGTACTTGCAGTTCAATCTTAAAGTCATGTGTGAGCTGATCCAGCGGTTGATCT
TCCTCCCTCTGTGCTCCATCCTTTTCTGCCTGAGTTCTCCTTACCTGAGAGTGGTCAT
GAACCACTCATCACCTACTCTTCTGGAGGCTTCAGAGGAGCTACAGTGAAATAAAA
GCCGCATTGC (SEQ ID NO:211)

Translation:
STRCLPDGTSCLFSRIRCCGTCSSILKSCVS (SEQ ID NO:212)

Toxin Sequence:

Cys-Leu-Xaa3-Asp-Gly-Thr-Ser-Cys-Leu-Phe-Ser-Arg-Ile-Arg-Cys-Cys-Gly-Thr-Cys-Ser-Ser-Ile-Leu-Lys-Ser-Cys-Val-Ser-^ (SEQ ID NO:213)

Name: U010 homolog
Species: striatus
Cloned: Yes

DNA Sequence:

CGGCTTCTAATACGACTCACTATAGGGCAAGCAGTGGTAACAACGCAGAGTACGCG
GGGGGACGGCAGACCAGCTGGGGACCAGACAGACGTCAAACAGCATCGCAGTCAG
GTGTGGAGATCCCAAGACACCCAGAAGAAGGAGACAGAAGAGTTATCGTTCGTAAC
ACAATGGCCATGAACATGTCGATGACACTCTGCATGTTTGTAATGGTCGTCGTGGCA
GCCACTGTCATTGATTCCACTCAGTTACAAGAACCAGATCTCAGTCGCATGCGACGC
AGCGGGCCTGCTGACTGTTGCAGGATGAAAGAGTGTTGCACCGACAGAGTGAACGA
GTgTCTACAGCGCTATTCTGGCCGGGAAGATAAATTCGTTTCGTTTTGTTATCAGGA
GGCCACAGTCACATGTGGATCTTTTAACGAAATCGTGGGCTGTTGCTATGGATATCA
AATGTGCATGATACGAGTTGTGAAACCGAACAGTCTAAGTGGGGCCCATGAGGCGT
GCAAAACCGTTTCTTGTGGTAACCCTTGCGCTTGAGGTGTCCTCGCGCCACGTCACC
TGTGTACAGCGCCGTCACCAGAGCCCTGATCTTTATGCCCTTATCTGTCTTTTTGCTC
TTTCACTCTCTGAAGTCTTGAGGTTTGTTCCATTCTTGTCAATCATCTCACGCGCATC
CAAGTAAATAAAGGTGACGTGACAAAC (SEQ ID NO:214)

Translation:

MAMNMSMTLCMFVMVVVAATVIDSTQLQEPDLSRMRRSGPADCCRMKECCTDRVNE
CLQRYSGREDKFVSFCYQEATVTCGSFNEIVGCCYGYQMCMIRVVKPNSLSGAHEACK
TVSCGNPCA (SEQ ID NO:215)

Toxin Sequence:

Ser-Gly-Xaa3-Ala-Asp-Cys-Cys-Arg-Met-Lys-Xaa1-Cys-Cys-Thr-Asp-Arg-Val-Asn-Xaa1-Cys-Leu-Gln-Arg-Xaa5-Ser-Gly-Arg-Xaa1-Asp-Lys-Phe-Val-Ser-Phe-Cys-Xaa5-Gln-Xaa1-Ala-Thr-Val-Thr-Cys-Gly-Ser-Phe-Asn-Xaa1-Ile-Val-Gly-Cys-Cys-Xaa5-Gly-Xaa5-Gln-Met-Cys-Met-Ile-Arg-Val-Val-Lys-Xaa3-Asn-Ser-Leu-Ser-Gly-Ala-His-Xaa1-Ala-Cys-Lys-Thr-Val-Ser-Cys-Gly-Asn-Xaa3-Cys-Ala-^ (SEQ ID NO:216)

Name: WG002
Species: striatus
Isolated: Yes

Toxin Sequence:

Xaa4-Ser-Xaa4-Arg-Met-Gly-Asn-Gly-Asp-Arg-Arg-Ser-Asp-Gln-^ (SEQ ID NO:217)

Name: Sx8.1
Species: striolatus
Cloned: Yes

DNA Sequence:
ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTGACCCTGGCATCCA
GCCAGCAGGAGGGAGATGTCCAGGCAAGGAAAACAAGCCTGAAGAGCGACTTCTA
TCGTGCTCTGAGACCGTATGACAGACAGTGCACTTTTGTCAACAATTGTCAACAGAA
CGGTGCGTGTAACGGTGATTGCTCTTGCGGGGACCAGATTTGTAAATGCGGTTATAG
AATCAGTCCTGGGAGGTCAGGATGCGCGTGTACTTGTAGAAATGCCAAATGAATCA
CTTAACTCGTTGAAAGATTTTTAAAAATCCAGAGCTATATGTTCGAGAAAAACCGA
AGAC (SEQ ID NO:218)

Translation:
MMSKMGAMFVLLLLLTLASSQQEGDVQARKTSLKSDFYRALRPYDRQCTFVNNCQQN
GACNGDCSCGDQICKCGYRISPGRSGCACTCRNAK (SEQ ID NO:219)

Toxin Sequence:
Xaa2-Cys-Thr-Phe-Val-Asn-Asn-Cys-Gln-Gln-Asn-Gly-Ala-Cys-Asn-Gly-Asp-Cys-Ser-Cys-
Gly-Asp-Gln-Ile-Cys-Lys-Cys-Gly-Xaa5-Arg-Ile-Ser-Xaa3-Gly-Arg-Ser-Gly-Cys-Ala-Cys-Thr-
Cys-Arg-Asn-Ala-Lys-^ (SEQ ID NO:220)

Name: Ts6.3
Species: tessulatus
Cloned: Yes

DNA Sequence:
GGATCCATGAAACTGACGTGTGTGGTGATCATCGCCGTGCTGTTCCTGACGGCCTGT
CAATTCATTATAGCTGATTTCTCCAGAGATAAGCGGGTACATCGTGCAGAGAGGTTG
AGAGACATAATGCAGAATTTCAGAGGTACCAGGTCGTGCGCGGAATTTGGTGAAGT
TTGTAGTTCTACCGCTTGCTGCCCTGATTTGGATTGCGTTGAGGCCTATTCACCCATC
TGTCTCTGGGAATAGTCTGGCATCTGATATTTCCCGTCTGTGCTCTACCTACTTCTGC
CGGATTCATCCATACCTATGTGTGGCCATGAACCACTCAGTACCTACACCTCTGGTG
GCTTCCTAGGGACGTATATCAAAATAAAACCACATTGCAAAAAAAAAAAAAAAAA
(SEQ ID NO:221)

Translation:
MKLTCVVIIAVLFLTACQFIIADFSRDKRVHRAERLRDIMQNFRGTRSCAEFGEVCSSTA
CCPDLDCVEAYSPICLWE (SEQ ID NO:222)

Toxin Sequence:
Ser-Cys-Ala-Xaa1-Phe-Gly-Xaa1-Val-Cys-Ser-Ser-Thr-Ala-Cys-Cys-Xaa3-Asp-Leu-Asp-Cys-
Val-Xaa1-Ala-Xaa5-Ser-Xaa3-Ile-Cys-Leu-Xaa4-Xaa1-^ (SEQ ID NO:223)

Name: 4/43 SNX
Species: textile
Isolated: Yes
Cloned: Yes

DNA Sequence:
CGATTGCAGGGGTTaCGATGCGCCGTGTAGCTCTGGCGCGCCATGTTGTGATTGGTG
GACATGTTCAGCACGAACCAACCGCTGTTTTTAGGCTGACCACAAGCCATCCGACAT
CACCACTCTCCTCTTCAGAGGCTTCAAGGCTTTTTGTTCTCCTTTTGAAGAATCTTTA
CGAGTGAACAAACAAGTAGAATAGCACGTTTTTCCCCCTTTGAAAAATCAATAATG
GAGGTTAAACAAAACTGTCTTCTTCAATAAAGATTTTATCATAAT (SEQ ID NO:224)

Translation:
IQGGGDERQKAKINFLSRSDRDCRGYDAPCSSGAPCCDWWTCSARTNRCF (SEQ ID NO:225)

Toxin Sequence:
Asp-Cys-Arg-Gly-Xaa5-Asp-Ala-Xaa3-Cys-Ser-Ser-Gly-Ala-Xaa3-Cys-Cys-Asp-Xaa4-Xaa4-Thr-Cys-Ser-Ala-Arg-Thr-Asn-Arg-Cys-Phe-^ (SEQ ID NO:226)

Name: convulsion
Species: textile
Isolated: Yes

Toxin Sequence:
Asn-Cys-Xaa3-Xaa5-Cys-Val-Val-Xaa5-Cys-Cys-Xaa3-Xaa3-Ala-Xaa5-Cys-Xaa1-Ala-Ser-Gly-Cys-Arg-Xaa3-Xaa3-# (SEQ ID NO:227)

Name: Tx1.6
Species: textile
Cloned: Yes

DNA Sequence:
ATGCACTGTCTCCCAATCTTCGTCATTCTTCTGCTGCTGACTGCATCTGGACCTAGCG
TTGATGCCCAACTGAAGACCAAAGATGATGTGCCCCTGTCATCTTTCCGAGATCATG
CAAAGAGTACCCTACGAAGACTTCAGGACAAACAGACTTGCTGTGGCTATAGGATG
TGTGTTCCTTGTGGTTAACCAGCATGAAGGATCC (SEQ ID NO:228)

Translation:
MHCLPIFVILLLLTASGPSVDAQLKTKDDVPLSSFRDHAKSTLRRLQDKQTCCGYRMCV PCG (SEQ ID NO:229)

Toxin Sequence:
Xaa2-Thr-Cys-Cys-Gly-Xaa5-Arg-Met-Cys-Val-Xaa3-Cys-# (SEQ ID NO:230)

Name: Tx6.14
Species: textile
Cloned: Yes

DNA Sequence:
GTTATGGAGCGATTGCTATAGTTGGTTAGGATCATGTATTGCGCCCTCGCAGTGTTG
TTCTGAGGTTTGTGATTATTACTGCCGCCTATGGCGATGAACTCGGACCACAAGCCA
T (SEQ ID NO:231)

Translation:
LWSDCYSWLGSCIAPSQCCSEVCDYYCRLWR (SEQ ID NO:232)

Toxin Sequence:
Asp-Cys-Xaa5-Ser-Xaa4-Leu-Gly-Ser-Cys-Ile-Ala-Xaa3-Ser-Gln-Cys-Cys-Ser-Xaa1-Val-Cys-Asp-Xaa5-Xaa5-Cys-Arg-Leu-Xaa4-Arg-^ (SEQ ID NO:233)

Name: Tx6.3
Species: textile
Cloned: Yes

DNA Sequence:
AGCTGACGAATGAAAAATTCCGAGAATGTCAAGCTCAGCAAGAGAAAATGTGTGGA
ACAATGGAAATACTGCACCCGAGAGTCCTTATGTTGCGCGGGTTTGTGTTTGTTTAG
TTTCTGCATTCTATAACGCTAATCCAGAGTCGTATATTCCGTCTAAGCTCCACCTGGC
ACTGTCTGGTATGTTCCTGCCAGTGACTGGTCTCATACCGCTTAGACTCTGGTCCGTC
TTCTCTGCAACCACAGGAGAACGTGCATTATTACAATAAACGCATACTGC (SEQ ID NO:234)

Translation:
RMKNSENVKLSKRKCVEQWKYCTRESLCCAGLCLFSFCIL (SEQ ID NO:235)

Toxin Sequence:
Lys-Cys-Val-Xaa1-Gln-Xaa4-Lys-Xaa5-Cys-Thr-Arg-Xaa1-Ser-Leu-Cys-Cys-Ala-Gly-Leu-Cys-Leu-Phe-Ser-Phe-Cys-Ile-Leu-^ (SEQ ID NO:236)

Name: Tx6.7
Species: textile
Cloned: Yes

DNA Sequence:

CAGAGCCGCTCTGGTGTGCAGACCTGTCTCCAGCCCTCCGTCTCCCTGATCGGTGGT
TCTGCCTGCATAGCTGTCTTCTCCACGAAGCTTTCCACAGGTATAAATAACGCTTCA
GTCTCCCGTCCTGTATTGGGCCGCCGTTACAAGCCAGACCGATACAGCCAGGTCCA
GTCTACTTTGCGAGTGAGTTAAAAGCTCCAGCATTCTACCAGCATCACCAGAATGAA
GGTGAGCAGCGTGCTGATCGTGGCTACGCTGACACTGACCGCAGGCCAGCTGGTTA
GTGCTTCTTCCCATTACTCAAAAGATGTCCAGATTCTTCCTTCTGTGAGATCAGCTGA
CGAAgTGGAAAATTCCGAGAATGTCAGGCTCAGCAAGAGAAGATGTGTGGAACAAT

GGGAAGTCTGCGGCATAATCTTGTTCTCCTCATCATGTTGCGGGCAGTTGTGTTTGTT TGGTTTCTGCGTTCTATAACGCTAATCCAGAGTCGTATATTCCGTCTAAGCTCCA (SEQ ID NO:237)

Translation:
MKVSSVLIVATLTLTAGQLVSASSHYSKDVQILPSVRSADEVENSENVRLSKRRCVEQW EVCGIILFSSSCCGQLCLFGFCVL (SEQ ID NO:238)

Toxin Sequence:
Cys-Val-Xaa1-Gln-Xaa4-Xaa1-Val-Cys-Gly-Ile-Ile-Leu-Phe-Ser-Ser-Ser-Cys-Cys-Gly-Gln-Leu-Cys-Leu-Phe-Gly-Phe-Cys-Val-Leu-^ (SEQ ID NO:239)

Name: TxVIIA
Species: textile
Isolated: Yes

Toxin Sequence:
Cys-Gly-Gly-Xaa5-Ser-Thr-Xaa5-Cys-Xaa1-Val-Asp-Ser-Xaa1-Cys-Cys-Ser-Asp-Asn-Cys-Val-Arg-Ser-Xaa5-Cys-Thr-Leu-Phe-# (SEQ ID NO:240)

Name: U030
Species: textile
Isolated: Yes

Toxin Sequence:
Gly-Cys-Asn-Asn-Ser-Cys-Gln-Xaa1-His-Ser-Asp-Cys-Xaa1-Ser-His-Cys-Ile-Cys-Thr-Ser-Arg-Gly-Cys-Gly-Ala-Val-Asn-# (SEQ ID NO:241)

Name: Bromosleeper-T1
Species: tulipa
Cloned: Yes

DNA Sequence:
CAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCTTCT ACTTCTTGTGTCCATGGCAACCAGTCATCGTTATGCAAGAGAAAAGCAGGCGACGC GAAGGGACGCAGTCAACGTCAGACGGAGAAGCAGACCAAAAACAAAGGAGTGCGA AAGGTACTGTGAGCTGGAGGAAAAGCACTGCTGCTGCATAAGAAGTAACGGACCCA AATGTTCCAGAATATGCATATTCAAATTTTGGTGTTAGTTTTCTGTACACTGTCCATT CATTATCTTATCAGTACAAGTGTAAACGAGACATGTCAGAAAGTCGAAGGTTGTGC GTAATTTGATAAGCATTGTTTACTGGGACGAACGGA (SEQ ID NO:242)

Translation:
MSGLGIMVLTLLLLVSMATSHRYAREKQATRRDAVNVRRRSRPKTKECERYCELEEKH CCCIRSNGPKCSRICIFKFWC (SEQ ID NO:243)

Toxin Sequence:

Xaa3-Lys-Thr-Lys-Xaa1-Cys-Xaa1-Arg-Xaa5-Cys-Xaa1-Leu-Xaa1-Xaa1-Lys-His-Cys-Cys-Cys-Ile-Arg-Ser-Asn-Gly-Xaa3-Lys-Cys-Ser-Arg-Ile-Cys-Ile-Phe-Lys-Phe-Xaa4-Cys-^ (SEQ ID NO:244)

Name: Bromosleeper-T2
Species: tulipa
Cloned: Yes

DNA Sequence:
CAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCTTCT
CCTTCTTGTGCTAATGACAACCAGTCATCAGGATGCAGGAGAGAAGCAGGCGATGC
AAAGGGACGCAAAGAACTTCAGTCGGAGAAGATTAGTCATTCGGAGACCAAAAAC
AAGGGAGTGCGAAATGCAGTGTGAGCAGGAGGAGAAACACTGCTGCCGCGTAAGA
GATGGTACGGGCCAATGTGCCCCTAAGTGCTTGGGAATTAACTGGTAGTTTCTGTAC
ACTGTCTCATTCATTATCTTATCAGTACACGTGTAACGAGACATGTCAGAAAGTCGA
AGGTAGTGCGTAATTTGATAAGCATTGTTTACTGGGACGAACGGA (SEQ ID NO:245)

Translation:
MSGLGIMVLTLLLLVLMTTSHQDAGEKQAMQRDAKNFSRRRLVIRRPKTRECEMQCEQ
EEKHCCRVRDGTGQCAPKCLGINW (SEQ ID NO:246)

Toxin Sequence:
Xaa3-Lys-Thr-Arg-Xaa1-Cys-Xaa1-Met-Gln-Cys-Xaa1-Gln-Xaa1-Xaa1-Lys-His-Cys-Cys-Arg-Val-Arg-Asp-Gly-Thr-Gly-Gln-Cys-Ala-Xaa3-Lys-Cys-Leu-Gly-Ile-Asn-Xaa4-^ (SEQ ID NO:247)

Name: T8.1
Species: tulipa
Cloned: Yes

DNA Sequence:
ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCACCCTGGCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAACACGCCTGAAGAGCGACTTCTA
TCGTGCTCTGCCAAGGTTTGGCCCAATATGCACTTGTTTTAAAAGCCAGAACTGTCG
GGGTTCTTGTGAATGCATGTCACCTCCCGGTTGTTACTGCAGTAACAATGGCATTCG
TGAACGAGGATGCTCGTGTACATGTCCAGGGACTGGTTGAATGATTTGAAAAATTC
AGAGCAATATGTTGCAGAAAAACCGAAGACCGAGACTTCTCACAATAAATCCATAA
AGACATTAAAAAAAAAAAAAAAAA (SEQ ID NO:248)

Translation:
MMSKMGAMFVLLLLFTLASSQQEGDVQARKTRLKSDFYRALPRFGPICTCFKSQNCRG
SCECMSPPGCYCSNNGIRERGCSCTCPGTG (SEQ ID NO:249)

Toxin Sequence:
Phe-Gly-Xaa3-Ile-Cys-Thr-Cys-Phe-Lys-Ser-Gln-Asn-Cys-Arg-Gly-Ser-Cys-Xaa1-Cys-Met-Ser-Xaa3-Xaa3-Gly-Cys-Xaa5-Cys-Ser-Asn-Asn-Gly-Ile-Arg-Xaa1-Arg-Gly-Cys-Ser-Cys-Thr-Cys-Xaa3-Gly-Thr-# (SEQ ID NO:250)

Name: T8.2
Species: tulipa
Cloned: Yes

DNA Sequence:
ATGATGTCGAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTCACCCTGGCATCCA
GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAACACGCCTGAAGAGCGACTTCTA
TCGTACTCTGGCAATATCTGACAGAGGATGCACTGGCAACTGTGATTGGACGTGTA
GCGGTGATTGCAGCTGCCAGGGCACATCTGACTCGTGTCACTGCATTCCACCAAAAT
CAATAGGCAACAGATGCCGGTGTCAGTGTAAAAGAAAAATCGAAATTGACTGATTC
TTTTAACTCGTTGAACGATTTAAAAATCAGACCAATATGTAGGCAGAAAACCGAAG
ACTCTGAGACTCTCGTAATAATCGTAAGCAAAAAAAAAAAAAAAA (SEQ ID NO:251)

Translation:
MMSKMGAMFVLLLLFTLASSQQEGDVQARKTRLKSDFYRTLAISDRGCTGNCDWTCS
GDCSCQGTSDSCHCIPPKSIGNRCRCQCKRKIEID (SEQ ID NO:252)

Toxin Sequence:
Gly-Cys-Thr-Gly-Asn-Cys-Asp-Xaa4-Thr-Cys-Ser-Gly-Asp-Cys-Ser-Cys-Gln-Gly-Thr-Ser-Asp-Ser-Cys-His-Cys-Ile-Xaa3-Xaa3-Lys-Ser-Ile-Gly-Asn-Arg-Cys-Arg-Cys-Gln-Cys-Lys-Arg-Lys-Ile-Xaa1-Ile-Asp-^ (SEQ ID NO:253)

Name: Vr6.1
Species: virgo
Cloned: Yes

DNA Sequence:
GGATCCATGAAACTGACGTGTGTGGTGATCATCACTGTGCTGTTCCTGACGGCCAGT
CAGCTCATTACAGCTGATTACTCCAGAGATCAGCGGCAGTACCGTGCAGTGAGGTT
GGGAGATGAAATGCGGAATTTCAAAGGTGCCAGGGACTGCGGGGGACAAGGTGAA
GGTTGTTATACTCAACCTTGCTGCCCTGGTCTGCGGTGCCGTGGCGGCGGTACTGGA
GGAGGCGTATGCCAGCTGTAGTAATAGTTTGGCATCTGATATTTCCCCTCTGTGCTC
CACCCTCTTTTGCCTGATTCATCCTTACCTATGTGTGGTCATGAACCACTCAGTAGCT
ACACCTCTGGTGGATTCAGAGAACGTATATCAAAATAAAACCACATTGCAATAAAA
AAAAAAAA (SEQ ID NO:254)

Translation:
MKLTCVVIITVLFLTASQLITADYSRDQRQYRAVRLGDEMRNFKGARDCGGQGEGCYT
QPCCPGLRCRGGGTGGGVCQL (SEQ ID NO:255)

Toxin Sequence:
Asp-Cys-Gly-Gly-Gln-Gly-Xaa1-Gly-Cys-Xaa5-Thr-Gln-Xaa3-Cys-Cys-Xaa3-Gly-Leu-Arg-Cys-Arg-Gly-Gly-Gly-Thr-Gly-Gly-Gly-Val-Cys-Gln-Leu-^ (SEQ ID NO:256)

Name: R6.9
Species: radiatus

Cloned: Yes

DNA Sequence:
ATCATGCAGAAACTGACAATCCTGCTTCTTGTTGCTGCTATACTGATGTCGACCCAG
GTCCTGATTCAAGGTGGTGGAGAAAAACGCCAAAAAGTCAACATTTTTTCAAAAAG
AAAGACAGATGCTGAGACCTGGTGGGAGGGCGAATGCTCTAATTGGTTAGGAAGTT
GTTCGACGCCCTCAAATTGCTGTCTCAAGAGTTGTAATGGGCACTGCACATTGTGGT
GATGAACTCTGACCACAAAGCCATCCAACATCACCGCTCTCCTCTTCAGAGTCTTCA
AG (SEQ ID NO:257)

Translation:
MQKLTILLLVAAILMSTQVLIQGGGEKRQKVNIFSKRKTDAETWWEGECSNWLGSCST
PSNCCLKSCNGHCTLW (SEQ ID NO:258)

Toxin Sequence:
Xaa4-Xaa4-Xaa1-Gly-Xaa1-Cys-Ser-Asn-Xaa4-Leu-Gly-Ser-Cys-Ser-Thr-Xaa3-Ser-Asn-Cys-
Cys-Leu-Lys-Ser-Cys-Asn-Gly-His-Cys-Thr-Leu-Xaa4-^ (SEQ ID NO:259)

Name: R6.10
Species: radiatus
Cloned: Yes

DNA Sequence:
ATCATGCAGAAACTGATAATCCTGCTTCTTGTTGCTGCTGTACTGATGTCCACCCAG
GCCCTGATTCAAGGTGGTGGAGGAAAACGCCAACAGGCAAAGAGCAAGTATTTTTC
CGAAAGAAAGGCACCTGCTAAGCGTTGGTTTGGACACGAAGAATGCACTTATTGGT
TGGGGCCTTGTGAGGTGGACGACACGTGTTGTTCTGCCAGTTGTGAGTCCAAGTTCT
GCGGGTTGTGGTGATGGACACTGACCACAAGTCATCCTACATCGCCACTCTCCTGTT
CAGAGTCTTCAAG (SEQ ID NO:260)

Translation:
MQKLIILLLVAAVLMSTQALIQGGGGKRQQAKSKYFSERKAPAKRWFGHEECTYWLGP
CEVDDTCCSASCESKFCGLW (SEQ ID NO:261)

Toxin Sequence:
Xaa4-Phe-Gly-His-Xaa1-Xaa1-Cys-Thr-Xaa5-Xaa4-Leu-Gly-Xaa3-Cys-Xaa1-Val-Asp-Asp-
Thr-Cys-Cys-Ser-Ala-Ser-Cys-Xaa1-Ser-Lys-Phe-Cys-Gly-Leu-Xaa4-^ (SEQ ID NO:262)

Name: Wi6.1
Species: wittigi
Cloned: Yes

DNA Sequence:
GGATCCATGAAACTGACGTGTGTGGTGATCATCGCCTTGCTGTTCCTGACGGCCTGT
CAGCTCATTACGGCTGATTACTCCAGAGATGAGCAGTCTGGCAGTACAGTGCGGTTT
CTAGACAGACCACGGCGTTTTGGTTCGTTCATACCGTGCGCCCGTTTAGGTGAACCA

TGTACCATATGCTGCCGTCCTTTGAGGTGCCGTGAAAGCGGAACACCCACATGTCAA
GTGTGATTGTCTGGCATCTGATATTTCCCCTCTGTGCCCTACCCTCTTTTGCCTGAGT
CATCCATACCTGTGCTCGAG (SEQ ID NO:263)

Translation:
MKLTCVVIIALLFLTACQLITADYSRDEQSGSTVRFLDRPRRFGSFIPCARLGEPCTICCRP
LRCRESGTPTCQV (SEQ ID NO:264)

Toxin Sequence:
Phe-Gly-Ser-Phe-Ile-Xaa3-Cys-Ala-Arg-Leu-Gly-Xaa1-Xaa3-Cys-Thr-Ile-Cys-Cys-Arg-Xaa3-Leu-Arg-Cys-Arg-Xaa1-Ser-Gly-Thr-Xaa3-Thr-Cys-Gln-Val-^ (SEQ ID NO:265)

Name: Rg6.6
Species: regius
Cloned: Yes

DNA Sequence:
GGATCCATGAAACTGACGTGCGTGGTGATCATGGCCTCGCTGTTCCTGGCGGCCTGT
CAATTCCTTACAGCTGGAGGTGACTCAAGAAGTAAGCAGCGGTATCCTGATTGGAG
GCTGGGCTACCGAAAGTCCAAGTTGATGGCTAAGAAGACGTGCCTGGAACATAACA
AACTATGTTGGTATGATAGAGACTGCTGCACCATATATTGTAATGAAAACAAATGC
GGCGTGAAACCTCAATGAATGTTTCACACACACACACACACACACACACACACACA
CACACACACACACACACACACACACACACACATCTGGCGTCTGACCATTCCCCCTCTGT
GCTCTATCCTCTTGTTCCTGAGTCATCCATACCTGTGCTCGAG (SEQ ID NO:266)

Translation:
MKLTCVVIMASLFLAACQFLTAGGDSRSKQRYPDWRLGYRKSKLMAKKTCLEHNKLC
WYDRDCCTIYCNENKCGVKPQ (SEQ ID NO:267)

Toxin Sequence:
Thr-Cys-Leu-Xaa1-His-Asn-Lys-Leu-Cys-Xaa4-Xaa5-Asp-Arg-Asp-Cys-Cys-Thr-Ile-Xaa5-Cys-Asn-Xaa1-Asn-Lys-Cys-Gly-Val-Lys-Xaa3-Gln-^ (SEQ ID NO:268)

Name: R6.9
Species: radiatus
Cloned: Yes

DNA Sequence:
ATCATGCAGAAACTGACAATCCTGCTTCTTGTTGCTGCTATACTGATGTCGACCCAG
GTCCTGATTCAAGGTGGTGGAGAAAAACGCCAAAAAGTCAACATTTTTTCAAAAAG
AAAGACAGATGCTGAGACCTGGTGGGAGGGCGAATGCTCTAATTGGTTAGGAAGTT
GTTCGACGCCCTCAAATTGCTGTCTCAAGAGTTGTAATGGGCACTGCACATTGTGGT
GATGAACTCTGACCACAAAGCCATCCAACATCACCGCTCTCCTCTTCAGAGTCTTCA
AG (SEQ ID NO:269)

Translation:
MQKLTILLLVAAILMSTQVLIQGGGEKRQKVNIFSKRKTDAETWWEGECSNWLGSCST
PSNCCLKSCNGHCTLW (SEQ ID NO:270)

Toxin Sequence:
Xaa4-Xaa4-Xaa1-Gly-Xaa1-Cys-Ser-Asn-Xaa4-Leu-Gly-Ser-Cys-Ser-Thr-Xaa3-Ser-Asn-Cys-Cys-Leu-Lys-Ser-Cys-Asn-Gly-His-Cys-Thr-Leu-Xaa4-^ (SEQ ID NO:271)

Name: R6.10
Species: radiatus
Isolated: Yes
Cloned: Yes

DNA Sequence:
ATCATGCAGAAACTGATAATCCTGCTTCTTGTTGCTGCTGTACTGATGTCCACCCAG
GCCCTGATTCAAGGTGGTGGAGGAAAACGCCAACAGGCAAAGAGCAAGTATTTTTC
CGAAAGAAAGGCACCTGCTAAGCGTTGGTTTGGACACGAAGAATGCACTTATTGGT
TGGGGCCTTGTGAGGTGGACGACACGTGTTGTTCTGCCAGTTGTGAGTCCAAGTTCT
GCGGGTTGTGGTGATGGACACTGACCACAAGTCATCCTACATCGCCACTCTCCTGTT
CAGAGTCTTCAAG (SEQ ID NO:272)

Translation:
MQKLIILLLVAAVLMSTQALIQGGGGKRQQAKSKYFSERKAPAKRWFGHEECTYWLGP
CEVDDTCCSASCESKFCGLW (SEQ ID NO:273)

Toxin Sequence:
Xaa4-Phe-Gly-His-Xaa1-Xaa1-Cys-Thr-Xaa5-Xaa4-Leu-Gly-Xaa3-Cys-Xaa1-Val-Asp-Asp-Thr-Cys-Cys-Ser-Ala-Ser-Cys-Xaa1-Ser-Lys-Phe-Cys-Gly-Leu-Xaa4-^ (SEQ ID NO:274)

Name: Sf 5.1
Species: spurius
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGC
TGATTCCATCTGCACCTAGCACTGATGCCCGACCGAAGACCAAAGATGATGTGCGC
CTGGCATCTTTCCACGGTAAGGCAAAGCGAACCCTACAAATACCTAGGGGGAATAT
CCACTGTTGCACAAAATATCAGCCGTGCTGTTCTTCACCATCATAAAGGGAAATGAC
TTTGATGAGACCCCTGCGAACTGTCCCTGGATGTGAAATTTGGAAACGAGACTGTTC
CTTTCGCGCGTGTTCGTGGAATTTCGAATGGTCGTTAATAACACGCTGCCTCTTGCA
AACTACAATCTCTCTGTCCTTTATCTGTGGACTGGATGTCAACACTG (SEQ ID NO:275)

Translation:

MRCLPVFVILLLLIPSAPSTDARPKTKDDVRLASFHGKAKRTLQIPRGNIHCCTKYQPCC SSPS (SEQ ID NO:276)

Toxin Sequence:
Gly-Asn-Ile-His-Cys-Cys-Thr-Lys-Xaa5-Gln-Xaa3-Cys-Cys-Ser-Ser-Xaa3-Ser-^ (SEQ ID NO:277)

Name: Nb5.1
Species: nobilis
Cloned: Yes

DNA Sequence:
ATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGCTGACTGCATCTGCACCAAGCG
TTGATGCCCGACCGAAGACCAAAGATGATGTGCTCCGGGCATCTTTCCGCGATAAT
GCAAAGAGTACCCTACAAAGACTTTGGAACAAACGCATCTGCTGCCCCATAATTCTT
TGGTGCTGTGGTTAACCAGCATGAAGTTCCCAGGA (SEQ ID NO:278)

Translation:
MRCLPVFVILLLLTASAPSVDARPKTKDDVLRASFRDNAKSTLQRLWNKRICCPIILWCC G (SEQ ID NO:279)

Toxin Sequence:
Ile-Cys-Cys-Xaa3-Ile-Ile-Leu-Xaa4-Cys-Cys-# (SEQ ID NO:280)

Name: Bt5.1
Species: betulinus
Cloned: Yes

DNA Sequence:
ATGCGCTGTCTCCCAGTCTTCATCATTCTTCTGGTGCTGATTGCATCTGCACCTACCG
TTGATGCCCGACCAAAGATCGAAGATGATGAGTCCCTGGCATCTTTCCATGNTCATN
AACCACCATNANNGNTNCANCTTTTGAACAAACGCAATTGCTGCCCAGACTCTCCTC
CGTGCTGTCATTAACCAGCATGAAGGTTCAGGA (SEQ ID NO:281)

Translation:
MRCLPVFIILLVLIASAPTVDARPKIEDDESLASFH?H?PP????LLNKRNCCPDSPPCCH (SEQ ID NO:282)

Toxin Sequence:
Asn-Cys-Cys-Xaa3-Asp-Ser-Xaa3-Xaa3-Cys-Cys-His-^ (SEQ ID NO:283)

Name: t-PVA
Species: purpurascens
Isolated: Yes

Cloned: Yes

DNA Sequence:
GGAATTCCAAATGATGTAATTACTGACTACATGGTCATAGTGTATACCCATTGAAAA
ATTTCTATGACATTTCAGTTGTTAGATCATCCAGTTCCACAGATGGAAAGACAGAGA
GATAGTAGCTTGCAAGTGGCAGCGTGTTGTTAACGACCATTCGACATTCCATGAACA
CGTGTGAAAGGAGCAGTCTGCTTTCCAAATCTGACATCCAGGGACAGTTTGCAGGG
GTCTCATCCAAAGTCATCTTCCTTTATCCCAAAGTACAGCACCGCATCTGTTTTGGA
CAGCAACCGCGTTTCTTCCAAAATCTTTGTAGGGTTCCTTTTGCATTATCGTGGAAA
GATGCCAGGGGCATATCATCTTTGGTCTTCGGATGAGCATCAACGCAAGGTGCAGA
TGGAATCAGCAGCAGAAGAATGACGAAGACTGGCAGACAGCGCATTCTGCTTGTAG
TCAGCTTCCGAATTCCAAGCCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTC
GAGCATGCATCTAGAGGGCCCAATTCGCCCTATAGTGAGTCGTATGACAATTCAcTG
GC (SEQ ID NO:284)

Translation:
MRCLPVFVILLLLIPSAPCVDAHPKTKDDMPLASFHDNAKGTLQRFWKKRGCCPKQMR
CCTLG (SEQ ID NO:285)

Toxin Sequence:
Gly-Cys-Cys-Xaa3-Lys-Gln-Met-Arg-Cys-Cys-Thr-Leu-# (SEQ ID NO:286)

Name: Af5.2
Species: ammiralis
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCACTGTCTCCCAGTCGTCGTCATTCTTCTGCTGC
TGACTGCATCTGGTGGACCTAGCGTTGATGCCCGACTGAAGACCAAAGATGATGTG
CCCCTGTCATCTTTCCGCGATAATACAAAGAGTATCCTACAAAGACTTTGGAAGCGA
GGCAACTGCTGTGAATTTTGGGAGTTTTGCTGTGATTAACCAGCATGAAGG (SEQ ID
NO:287)

Translation:
MHCLPVVVILLLLLTASGGPSVDARLKTKDDVPLSSFRDNTKSILQRLWKRGNCCEFWEF
CCD (SEQ ID NO:288)

Toxin Sequence:
Gly-Asn-Cys-Cys-Xaa1-Phe-Xaa4-Xaa1-Phe-Cys-Cys-Asp-^ (SEQ ID NO:289)

Name: Da5.1
Species: dalli
Cloned: Yes

DNA Sequence:

GGAAGCTGACTACAAGCAGAATGCACTGTCTCCCAGTCTTCGTCATTCTTCTGCTGC
TGACTGCATCTGGACCTAGCGTTGATGCCCAACCGAAGACCGAAGTTGATGTGCCC
CTGTCATCTTTCCGCGATAATGCAAAGCGTGCCCTACAAAGACTTCCGCGTTGCTGT
GAATATTGGAAGTTGTGCTGTGGTTAACCAGCATGAAGG (SEQ ID NO:290)

Translation:
MHCLPVFVILLLLTASGPSVDAQPKTEVDVPLSSFRDNAKRALQRLPRCCEYWKLCCG
(SEQ ID NO:291)

Toxin Sequence:
Cys-Cys-Xaa1-Xaa5-Xaa4-Lys-Leu-Cys-Cys-# (SEQ ID NO:292)

Name: Om5.1
Species: omaria
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGC
TAACTGCATCTGCACCTAGCGTTGATGCCCGACCGAAGGCCAAAGATGATGTGCCC
CTGGCATCTTTCCGTGATAATGCAAAGAGTACCCTACAAAGACTTCAGGACAAACG
CGTTTGCTGTGGCTATAAGTTTTTTTGCTGTCGTTAACCAGCATGAAGG (SEQ ID
NO:293)

Translation:
MRCLPVFVILLLLTASAPSVDARPKAKDDVPLASFRDNAKSTLQRLQDKRVCCGYKFFC
CR (SEQ ID NO:294)

Toxin Sequence:
Val-Cys-Cys-Gly-Xaa5-Lys-Phe-Phe-Cys-Cys-Arg-^ (SEQ ID NO:295)

Name: Au5.1
Species: aulicus
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGC
TGACTGCATCTGCACCTAACGTTGATGCCCAACCGAAGACCAAAGATGATGTGCCC
CTGGCATCTTTGCACGATGATGCAAAGAGTGCACTACAACATTGGAACCAACGCTG
CTGCCCCATGATCTATTGGTGCTGTAGTTAACCAGCATGAAGG (SEQ ID NO:296)

Translation:
MRCLPVFVILLLLTASAPNVDAQPKTKDDVPLASLHDDAKSALQHWNQRCCPMIYWC
CS (SEQ ID NO:297)

Toxin Sequence:

Cys-Cys-Xaa3-Met-Ile-Xaa5-Xaa4-Cys-Cys-Ser-^ (SEQ ID NO:298)

Name: Au5.4
Species: aulicus
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCACTGTCTCCCAGTCTTCGTCATTCTTCTGCTGC
TGACTGCATCTGCACCTAACGTTGATGCCCAACCGAAGACCAAAGATGATGTGCCC
CTGGCATCTTTGCACGATGATGCAAAGAGTGCACTACAACATTGGAACCAACGCTG
CTGCCCCGAGATCTATTGGTGCTGTAGTTAACCAGCATGAAGG (SEQ ID NO:299)

Translation:
MHCLPVFVILLLLTASAPNVDAQPKTKDDVPLASLHDDAKSALQHWNQRCCPEIYWCC
S (SEQ ID NO:300)

Toxin Sequence:
Cys-Cys-Xaa3-Xaa1-Ile-Xaa5-Xaa4-Cys-Cys-Ser-^ (SEQ ID NO:301)

Name: Af5.1
Species: ammiralis
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGC
TGATTGCATCTGCACCTAGCGTTGATGCCCAACCGAAGACCAAAGATGATGTGTCCC
TGGCATCTTTGCACGATAATATAAAGAGTACTCTACAAACACTTTGGAACAAACGCT
GCTGCCCCCCTGTGATTTGGTGCTGTGGTTAACCAGCATAAAGG (SEQ ID NO:302)

Translation:
MRCLPVFVILLLLIASAPSVDAQPKTKDDVSLASLHDNIKSTLQTLWNKRCCPPVIWCCG
(SEQ ID NO:303)

Toxin Sequence:
Cys-Cys-Xaa3-Xaa3-Val-Ile-Xaa4-Cys-Cys-# (SEQ ID NO:304)

Name: Au5.3
Species: aulicus
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGC
TGACTGCATCTGGACCTAGCGTTGATGCCCGACCGAAGACCAAAGATGATGTGCCT

CTGTCATCTTTCCGCGATAACGCAAAGAGTATCCTACAAAGACGTTGGAACAACTAT
TGCTGCACGAATGAGCTTTGGTGCTGTGGTTAACCAGCATGAAGG (SEQ ID NO:305)

Translation:
MRCLPVFVILLLLTASGPSVDARPKTKDDVPLSSFRDNAKSILQRRWNNYCCTNELWCC
G (SEQ ID NO:306)

Toxin Sequence:
Xaa4-Asn-Asn-Xaa5-Cys-Cys-Thr-Asn-Xaa1-Leu-Xaa4-Cys-Cys-# (SEQ ID NO:307)

Name: Da5.2
Species: dalli
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCACTGTCTCCCAGTCTTCGTCATTCTTCTGCTGC
TGACTGCATCTGGACCTAGCGTTGATGCCCGACCGAAGACCGAAGATGATGTGCCC
CTGTCATCTTTCCGCGATAATACAAAGAGTACCCTACAAAGACTTTTGAAGCCAGTC
AACTGCTGTCCTATTGATCAATCTTGCTGTTCTTAACCAGCATGAAGG (SEQ ID
NO:308)

Translation:
MHCLPVFVILLLLTASGPSVDARPKTEDDVPLSSFRDNTKSTLQRLLKPVNCCPIDQSCC
S (SEQ ID NO:309)

Toxin Sequence:
Xaa3-Val-Asn-Cys-Cys-Xaa3-Ile-Asp-Gln-Ser-Cys-Cys-Ser-^ (SEQ ID NO:310)

Name: Cn10.3
Species: consors
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCATCC
CTTCAGATCGTGCATCTGAAGGCAGGAATGCCGTAGTCCACGAGAGAGCGCCTGAG
CTGGTCGTTACGGCCACCACGACTTGCTGTGGTTATGATCCGATGACAATATGCCCT
CCTTGCATGTGCACTCATTCCTGTCCACCAAAAAGAAAACCAGGCCGCAGAAACGA
CTGATGCTCGAG (SEQ ID NO:311)

Translation:
MFTVFLLVVLATTVVSIPSDRASEGRNAVVHERAPELVVTATTTCCGYDPMTICPPCMC
THSCPPKRKPGRRND (SEQ ID NO:312)

Toxin Sequence:

Ala-Xaa3-Xaa1-Leu-Val-Val-Thr-Ala-Thr-Thr-Thr-Cys-Cys-Gly-Xaa5-Asp-Xaa3-Met-Thr-Ile-Cys-Xaa3-Xaa3-Cys-Met-Cys-Thr-His-Ser-Cys-Xaa3-Xaa3-Lys-Arg-Lys-Xaa3-# (SEQ ID NO:313)

Name: A10.2
Species: aurisiacus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCATCC
CTTCAGATCGTGCATCTGATGGCAGGAATGCCGCAGTCAACGAGAGACAATCTTGG
CTGGTCCCTTCGACAATCACGACTTGCTGTGGATATGATCCGGGGACAATGTGCCCT
CCTTGCAGGTGCAATAATACCTGTAAACCAAAAAAACCAAAACCAGGAAAAGGCC
GCAGAAACGACTGATGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:314)

Translation:
MFTVFLLVVLATTVVSIPSDRASDGRNAAVNERQSWLVPSTITTCCGYDPGTMCPPCRC
NNTCKPKKPKPGKGRRND (SEQ ID NO:315)

Toxin Sequence:
Xaa2-Ser-Xaa4-Leu-Val-Xaa3-Ser-Thr-Ile-Thr-Thr-Cys-Cys-Gly-Xaa5-Asp-Xaa3-Gly-Thr-Met-Cys-Xaa3-Xaa3-Cys-Arg-Cys-Asn-Asn-Thr-Cys-Lys-Xaa3-Lys-Lys-Xaa3-Lys-Xaa3-Gly-Lys-# (SEQ ID NO:316)

Name: Cn10.4
Species: consors
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCATCC
CTTCAGATCGTGCATCTGATGGCAGGAATGCCGTAGTCCACGAGAGAGCGCCTGAG
CTGGTCGTTACGGCCACCACGACTTGCTGTGGTTATGATCCGATGACATGGTGCCCT
TCTTGCATGTGCACTTATTCCTGTCCCCACCAAAGGAAAAAACCAGGCCGCAGAAA
CGACTGATGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:317)

Translation:
MFTVFLLVVLATTVVSIPSDRASDGRNAVVHERAPELVVTATTTCCGYDPMTWCPSCM
CTYSCPHQRKKPGRRND (SEQ ID NO:318)

Toxin Sequence:
Ala-Xaa3-Xaa1-Leu-Val-Val-Thr-Ala-Thr-Thr-Thr-Cys-Cys-Gly-Xaa5-Asp-Xaa3-Met-Thr-Xaa4-Cys-Xaa3-Ser-Cys-Met-Cys-Thr-Xaa5-Ser-Cys-Xaa3-His-Gln-Arg-Lys-Lys-Xaa3-# (SEQ ID NO:319)

Name: M10.3
Species: magus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCAGTGTCGTTTCCATCC
CTTCAGATCGTGCATCTGATGGCGGGAATGCCGTAGTCCACGAGAGAGCGCCTGAG
CTGGTCGTTACGGCCACCACGACTTGCTGTGGTTATGATCCGATGACAATATGCCCT
CCCTGCATGTGCACTCATTCCTGTCCACCAAAAGGAAAACCAGGCCGCAGGAACGA
CTGATGTCCAGGACCTCTGAACCACGACNCGAG (SEQ ID NO:320)

Translation:
MFTVFLLVVLATSVVSIPSDRASDGGNAVVHERAPELVVTATTTCCGYDPMTICPPCMC
THSCPPKGKPGRRND (SEQ ID NO:321)

Toxin Sequence:
Ala-Xaa3-Xaa1-Leu-Val-Val-Thr-Ala-Thr-Thr-Thr-Cys-Cys-Gly-Xaa5-Asp-Xaa3-Met-Thr-Ile-Cys-Xaa3-Xaa3-Cys-Met-Cys-Thr-His-Ser-Cys-Xaa3-Xaa3-Lys-Gly-Lys-Xaa3-# (SEQ ID NO:322)

Name: A10.3
Species: aurisiacus
Cloned: Yes

DNA Sequence:
GAATTCGCCCTTGAGGATCCGTGTGGTTCTGGGTCCAGAACCTGATGGCAGGAATG
CCGCAGTCAACGAGAGACAGAAATGGCTGGTCCATTCGAAAATCACGTATTGCTGT
GGTTATAATAAGATGGACATGTGCCCTCCTTGCATGTGCACTTATTCCTGTCCCCCC
CTAAAAAAAAAAAAGACCAGGCCGCAGAAACGACTGATGCTCCAGGACCCTCTGAA
CCACGACCTCGAGCGAAGGGCGAATTC (SEQ ID NO:323)

Translation:
VVLGPEPDGRNAAVNERQKWLVHSKITYCCGYNKMDMCPPCMCTYSCPPLKKKRPGR
RND (SEQ ID NO:324)

Toxin Sequence:
Xaa2-Lys-Xaa4-Leu-Val-His-Ser-Lys-Ile-Thr-Xaa5-Cys-Cys-Gly-Xaa5-Asn-Lys-Met-Asp-Met-Cys-Xaa3-Xaa3-Cys-Met-Cys-Thr-Xaa5-Ser-Cys-Xaa3-Xaa3-Leu-Lys-Lys-Lys-Arg-Xaa3-# (SEQ ID NO:325)

Name: A10.4
Species: aurisiacus
Cloned: Yes

DNA Sequence:
GAATTCGCCCTTGAGGATCCGTGTGGTTCTGGGTCCAGCATTTGATGGCAGGAATGC
CGCAGTCAACGAGAGAGCGCCTTGGACGGTCGTTACGGCCACCACGAATTGCTGCG
GTATTACCGGGCCAGGCTGCCTTCCTTGCCGTTGTACTCAAACATGTGGCTGATGCT
CCAGGACCCTCTGAACCACGACCTCGAGCGAAGGGCGAATTC (SEQ ID NO:326)

Translation:
VVLGPAFDGRNAAVNERAPWTVVTATTNCCGITGPGCLPCRCTQTCG (SEQ ID NO:327)

Toxin Sequence:
Ala-Xaa3-Xaa4-Thr-Val-Val-Thr-Ala-Thr-Thr-Asn-Cys-Cys-Gly-Ile-Thr-Gly-Xaa3-Gly-Cys-Leu-Xaa3-Cys-Arg-Cys-Thr-Gln-Thr-Cys-# (SEQ ID NO:328)

Name: Mr1.3
Species: marmoreus
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTCTTGATCATTCTTCTGCTGC
TGACTGCATCTGCACCTGGCGTTGTTGTCCTACCGAAGACCGAAGATGATGTGCCCA
TGTCATCTGTCTACGGTAATGGAAAGAGTATCCTACGAGGGATTCTGAGGAACGGT
GTTTGCTGTGGCTATAAGTTGTGCCTTCCATGTTAACCAGCATGAAGG (SEQ ID NO:329)

Translation:
MRCLPVLIILLLLTASAPGVVVLPKTEDDVPMSSVYGNGKSILRGILRNGVCCGYKLCLP C (SEQ ID NO:330)

Toxin Sequence:
Asn-Gly-Val-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-Leu-Xaa3-Cys-^ (SEQ ID NO:331)

Name: Pn1.5
Species: pennaceus
Cloned: Yes

DNA Sequence:
GGAATTCGGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTCTTCGTCATTCTT
CTGCTGCTGACTGCATCTGCACCTAGCGTTGATGCCAAAGTTCATCTGAAGACCAAA
GGTGATGGGCCCCTGTCATCTTTCCGAGATAATGCAAAGAGTACCCTACAAAGACTT
CAGGACAAAAGCACTTGCTGTGGCTTTAAGATGTGTATCCCTTGTAGTTAACCAGCA
TGAAGGATCC (SEQ ID NO:332)

Translation:

MRCLPVFVILLLLTASAPSVDAKVHLKTKGDGPLSSFRDNAKSTLQRLQDKSTCCGFKM CIPCS (SEQ ID NO:333)

Toxin Sequence:
Ser-Thr-Cys-Cys-Gly-Phe-Lys-Met-Cys-Ile-Xaa3-Cys-Ser-^ (SEQ ID NO:334)

Name: Pn1.6
Species: pennaceus
Cloned: Yes

DNA Sequence:
GAATTCGGAAGCTGACTACAAGCAGAATGCGTTGTCTCCCAGTCTTCGTCATTCTTC TGCTGCTGACTGCATCTGGACCTAGCGTTGATGCCCGACTGAAGACCAAAGATGAT GTGCCCCTGTCATCTTTCCGAGATAATGCAAAGAGTACCCTACAAAGACTTCAGGAC AAACGCCTTTGCTGTGGCTTTTGGATGTGTATTCCTTGTAATTAACCAGCATGAAGG ATCC (SEQ ID NO:335)

Translation:
MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRLQDKRLCCGFWMCI PCN (SEQ ID NO:336)

Toxin Sequence:
Leu-Cys-Cys-Gly-Phe-Xaa4-Met-Cys-Ile-Xaa3-Cys-Asn-^ (SEQ ID NO:337)

Name: Pn1.7
Species: pennaceus
Cloned: Yes

DNA Sequence:
GAATTCTCCCTTGGAATTCTGAAGCTGACTACAANCAGAATGCGTTGTCTCCCACTC TTCGTCATTCTTCTGCTGCTGACTGCATCTGGACCTACTGTTGATGCCCGACTGAAG ACCAAAGATGATGTGCCCCTGTCATCTTTCCGAGATAATGCAAAGAGTACCCTACA AAGACTTCAGGACAAAAGCACTTGCTGTGGCTTTAAGATGTGTATTCCTTGTGGTTA ACCAGCATGAAGGATCC (SEQ ID NO:338)

Translation:
MRCLPLFVILLLLTASGPTVDARLKTKDDVPLSSFRDNAKSTLQRLQDKSTCCGFKMCIP CG (SEQ ID NO:339)

Toxin Sequence:
Ser-Thr-Cys-Cys-Gly-Phe-Lys-Met-Cys-Ile-Xaa3-Cys-# (SEQ ID NO:340)

Name: Ep1.5
Species: episcopatus

Cloned: Yes

DNA Sequence:
GAATTCGCCCTTGGAATTCGGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTC TTCGTCATTCTTCTGCTGCTGACTGCATCTGGACCTANTGTTGATGCCAAAGTTCATC TGAAGACCAAAGGTGATGGCCCCTGTCATCTTTCCGAGATAATGCAAAGAGTACC CTACAAAGACTTCAGGACAAAAGCACTTGCTGTGGCTATAGGATGTGTGTTCCTTGT GGTTAACCAGCATGAAGGATCCV (SEQ ID NO:341)

Translation:
MRCLPVFVILLLLTASGPSVDAKVHLKTKGDGPLSSFRDNAKSTLQRLQDKSTCCGYR MCVPCG (SEQ ID NO:342)

Toxin Sequence:
Ser-Thr-Cys-Cys-Gly-Xaa5-Arg-Met-Cys-Val-Xaa3-Cys-# (SEQ ID NO:343)

Name: Mr1.1
Species: marmoreus
Isolated: Yes
Cloned: Yes

DNA Sequence:
GGCGAATACACCTGGCAGGTACTCAACGAACTTCAGGACACATTCTTTTCACCTGGA CACTGGAAACTGACAACAGGCAGAATGCGCTGTCTCCCAGTCTTGATCATTCTTCTG CTGCTGACTGCATCTGCACCTGGCGTTGTTGTCCTACCGAAGACCGAAGATGATGTG CCCATGTCATCTGTCTACGGTAATGGAAAGAGTATCCTACGAGGAATTCTGAGGAA CGGTGTTTGCTGTGGCTATAAGTTGTGCCATCCATGTTAACCAGCATGAAGGGAAAT GACTTTGGATGAGACCCCTGCGAACTGTCCCTGGATGTGAAATTTGGAAAGCAGAC TGTTCCTTTCGCACGTATTCGTGGAATTTCGAATGGTCGTAAACAACACGCTGCCAC TTGCAGGCTACTATCTCTCTGTCCTTTCATCTGTGGAAATGGATGATCTAACAACTG AAATATCAGAAATTTTTCAATGGCTATACACTATGACCATGTAGTCAGTAATTATAT CATTTGGACCTTTTGAAATATTTTTCAATATGTAAAGTTTTTGCACCCTGGAAAGGTC TTTTGGAGTTAAATATTTTAGTATGTTATGTTTTGCATACAAGTTATAGAATGCTGTC TTTCTTTTTGTTCCCACATCAATGGTGGGGGCAGAAATTATTTGTTTTGGTCAATGTA ATTATGACCTGCATTTAGTGCTATAGTGATTGCATTTTCAGCGTGGAATGTTTAATCT GCAAACAGAAAGTGGTTGATCGACTAATAAAGATTTGCATGGCACAAAAAAAAAA AAAAAAAGTACTCTGCGTTGTTACTCGAG (SEQ ID NO:344)

Translation:
MRCLPVLIILLLLTASAPGVVVLPKTEDDVPMSSVYGNGKSILRGILRNGVCCGYKLCHP C (SEQ ID NO:345)

Toxin Sequence:
Asn-Gly-Val-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-His-Xaa3-Cys-^ (SEQ ID NO:346)

Name: Mr1.2
Species: marmoreus
Isolated: Yes

Toxin Sequence:
Gly-Val-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-His-Xaa3-Cys-^ (SEQ ID NO:347)

Name: Bn1.5
Species: bandanus
Cloned: Yes

DNA Sequence:
ATGCGCTGTCTCCCAGTCTTGATCATTCTTCTGCTGCTGACTGCATCTGCACCTGGCG
TTGATGTCCTACCGAAGACCGAAGATGATGTGCCCCTGTCATCTGTCTACGATAATA
CAAAGAGTATCCTACGAGGACTTCTGGACAAACGTGCTTGCTGTGGCTACAAGCTTT
GCTCACCATGTTAACCAGCATGAAGGATCC (SEQ ID NO:348)

Translation:
MRCLPVLIILLLLTASAPGVDVLPKTEDDVPLSSVYDNTKSILRGLLDKRACCGYKLCSP
C (SEQ ID NO:349)

Toxin Sequence:
Ala-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-Ser-Xaa3-Cys-^ (SEQ ID NO:350)

Name: Au1.4
Species: aulicus
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGC
TGACTGCATCTGGACCTAGCGTTGATGCCCGACTGAAGACCAAAGATGATGTGCCC
CTGTCATCTTTCCGAGATAATGCAAAGAGTACCCTACAAAGACATCAGGACAAAAG
CGTTTGCTGTGGCTATAAGCTGTGTTTTCCTTGTGGTTAACCAGCATGAAGG (SEQ ID
NO:351)

Translation:
MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCF
PCG (SEQ ID NO:352)

Toxin Sequence:
Ser-Val-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-Phe-Xaa3-Cys-# (SEQ ID NO:353)

Name: Tx1.7
Species: textile

Cloned: Yes

DNA Sequence:
CAGGATCCAATGGGGTTTGTTGTGGCTATAGGATGTGTGTTCCTTGTGGTTAACCAG
CATGAAGGGAAATGACTTTGGATGAGACCCCTGCGAACTGTCCCTGGATGTGAGAT
TTGGAAAGCAGACTGTTCATTTTGCACGTGTTCGTGGAATTTCGAATGGTCGTTAAC
AACACGCTGCCACTTGCAAGCTACTATCTCTCTGTCCTTTTATCTGTGGAACTGTATG
ATCTAACAACTGAAATATCATANANATTTTTCAATGGGTATNCACTATGCATATGAT
CATGTAGGGTTCAAGGGGTCAAGATNC (SEQ ID NO:354)

Translation:
GSNGVCCGYRMCVPCG (SEQ ID NO:355)

Toxin Sequence:
Asn-Gly-Val-Cys-Cys-Gly-Xaa5-Arg-Met-Cys-Val-Xaa3-Cys-# (SEQ ID NO:356)

Name: Tx1.6
Species: textile
Cloned: Yes

DNA Sequence:
ATGCACTGTCTCCCAATCTTCGTCATTCTTCTGCTGCTGACTGCATCTGGACCTAGCG
TTGATGCCCAACTGAAGACCAAAGATGATGTGCCCCTGTCATCTTTCCGAGATCATG
CAAAGAGTACCCTACGAAGACTTCAGGACAAACAGACTTGCTGTGGCTATAGGATG
TGTGTTCCTTGTGGTTAACCAGCATGAAGGATCC (SEQ ID NO:357)

Translation:
MHCLPIFVILLLLTASGPSVDAQLKTKDDVPLSSFRDHAKSTLRRLQDKQTCCGYRMCV
PCG (SEQ ID NO:358)

Toxin Sequence:
Xaa2-Thr-Cys-Cys-Gly-Xaa5-Arg-Met-Cys-Val-Xaa3-Cys-# (SEQ ID NO:359)

Name: Af1.3
Species: ammiralis
Cloned: Yes

DNA Sequence:
AGAAGCTGACTACAAGCAGAATGCACTACCTCCCAGTCTTCGTCATTCTTCTGCTGC
TGACTGCATCTGGACCTAGCGTTGATGCCCAACTGAAGACCAAAGATGATGTGCCC
CTGTCATCTTTCCGAGATAATGCAAAGAGTACCCTACGAAGACTCCAGTACAAACA
GGCTTGCTGTGGCTTTAAGATGTGTGTTCCTTGTGGTTAACCAGCATGAAGG (SEQ
ID NO:360)

Translation:

MHYLPVFVILLLLTASGPSVDAQLKTKDDVPLSSFRDNAKSTLRRLQYKQACCGFKMC
VPCG (SEQ ID NO:361)

Toxin Sequence:
Xaa2-Ala-Cys-Cys-Gly-Phe-Lys-Met-Cys-Val-Xaa3-Cys-# (SEQ ID NO:362)

Name: Pn1.3
Species: pennaceus
Cloned: Yes

DNA Sequence:
ATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGCTGACTGCATCTGCACCTAGCG
TTGATGCCAAAGTTCATCTGAAGACCAAAGGTGATGGGCCCCTGTCATCTTTCCGAG
ATAATGCAAAGAGTACCCTACAAAGACTTCAGGACAAAAGCACTTGCTGTGGCTTT
AAGATGTGTATTCCTTGTCGTTAACCAGCATGAAGGATCC (SEQ ID NO:363)

Translation:
MRCLPVFVILLLLTASAPSVDAKVHLKTKGDGPLSSFRDNAKSTLQRLQDKSTCCGFKM
CIPCR (SEQ ID NO:364)

Toxin Sequence:
Ser-Thr-Cys-Cys-Gly-Phe-Lys-Met-Cys-Ile-Xaa3-Cys-Arg-^ (SEQ ID NO:365)

Name: Pn1.4
Species: pennaceus
Cloned: Yes

DNA Sequence:
CAGGATCCAATGGGGTTTGTTGTGGCTTTTGGATGTGTATTCCTTGTAATTAACCAG
CATGAAGGGAAATGACTTTGGATAAGACCCCTGCGAACTGTCCTTGGATGTGAGAT
TTGGAAAGCAGACTGTTCCTTTTGCACGTGTTCGTGGAATTTCGAATGGTCGTTAAC
AACACGCTGCCACTTGCAAGCTACTATCTCTCTGTCCTTTCATCTGTGGAACTGTATG
ATCTAACAACTGAAATATCATAGAAATTTTTCAATGGGTATACACTATGCATATGAC
CATGTANGGGTCAACAGNC (SEQ ID NO:366)

Translation:
GSNGVCCGFWMCIPCN (SEQ ID NO:367)

Toxin Sequence:
Asn-Gly-Val-Cys-Cys-Gly-Phe-Xaa4-Met-Cys-Ile-Xaa3-Cys-Asn-^ (SEQ ID NO:368)

Name: Om1.7
Species: omaria
Cloned: Yes

DNA Sequence:
GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGCTGACTGCATCTGCACCTAGCGTTGATGCCCGACCGAAGGCCAAAGATGATGTGCCCCTGTCATCTTTCCGTGATAATGCAAAGAGTACCCTACAAAGACTTCAGGACAAAGACGTTTGCTGTTACGTTAGAATGTGTCCTTGTCGTTAACCAGCATGAAGG (SEQ ID NO:369)

Translation:
MRCLPVFVILLLLTASAPSVDARPKAKDDVPLSSFRDNAKSTLQRLQDKDVCCYVRMCPCR (SEQ ID NO:370)

Toxin Sequence:
Asp-Val-Cys-Cys-Xaa5-Val-Arg-Met-Cys-Xaa3-Cys-Arg-^ (SEQ ID NO:371)

Name: Conophysin-R
Species: radiatus
Isolated: Yes

Toxin Sequence:
His-Xaa3-Thr-Lys-Xaa3-Cys-Met-Xaa5-Cys-Ser-Phe-Gly-Gln-Cys-Val-Gly-Xaa3-His-Ile-Cys-Cys-Gly-Xaa3-Thr-Gly-Cys-Xaa1-Met-Gly-Thr-Ala-Xaa1-Ala-Asn-Met-Cys-Ser-Xaa1-Xaa1-Asp-Xaa1-Asp-Xaa3-Ile-Xaa3-Cys-Gln-Val-Phe-Gly-Ser-Asp-Cys-Ala-Leu-Asn-Asn-Xaa3-Asp-Asn-Ile-His-Gly-His-Cys-Val-Ala-Asp-Gly-Ile-Cys-Cys-Val-Asp-Asp-Thr-Cys-Thr-Thr-His-Leu-Gly-Cys-Leu-^ (SEQ ID NO:372)

Name: Ts10.1
Species: tessulatus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTTGTTTCCTTCAGTGCAGATCGTGCCAACGTCAAAGCGTCTGACCTGATCGCCCAGGCCACCAGAGACGGCTGTCCACCACATCCCGTTCCTGGCATGCATAAGTGCATGTGTACTAATACATGTGGTTGAAGACGCTGATGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:373)

Translation:
MFTVFLLVVLATTVVSFSADRANVKASDLIAQATRDGCPPHPVPGMHKCMCTNTCG (SEQ ID NO:374)

Toxin Sequence:
Asp-Gly-Cys-Xaa3-Xaa3-His-Xaa3-Val-Xaa3-Gly-Met-His-Lys-Cys-Met-Cys-Thr-Asn-Thr-Cys-# (SEQ ID NO:375)

Name: G1.4
Species: geographus
Cloned: Yes

DNA Sequence:
ANNTAGANTNTGTCGTANTANNGGATCNTAANTANTGNNTCGANATGATNANGAGT
GATAAATGANNGGTGCACTNNTANTTANGNTNNTANGATNNNNATATTATNNTANN
NNNTAANANATATNGGTNNGGANNAAGAAGANTAAAAGTANNGNTTNGTGAAANA
ANGANNNNATGTTNNANNTCATAACNNNAATGTAAATAATANACGNNCCAGTGTG
AAANNNTNTCNNNNATAAAAATTCTNTNTNTNAANGTNNNTGTNTGNGTGTGTGTG
TGTGTGTGTGTGTGTGNGTGTGTGNGTGTGTGTGTGTGTGTGTGTGTGTGNGTGT
GTGTNTGTGNGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTNTGTGGTTCTGGGT
CCAGCATCTGATGNCAGGGATGACACAGCCAAAGACGAAGGGTCTNACATGGACA
AATTGGTCGAGAAAAAAGAATGTTGCCATCCTGCCTGTGGCAAACACTACAGTTGT
GGACGCTGATGCTCCAGGGTNTGAAGGANCAA (SEQ ID NO:376)

Translation:
SDXRDDTAKDEGSXMDKLVEKKECCHPACGKHYSCGR (SEQ ID NO:377)

Toxin Sequence:
Xaa1-Cys-Cys-His-Xaa3-Ala-Cys-Gly-Lys-His-Xaa5-Ser-Cys-# (SEQ ID NO:378)

Name: G1.5
Species: geographus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTGGTCTTGGCAACCACTGTCGTTTCCTTCC
CTTCAGAACGTGCATCTGATGGCAGGGATGACACAGCCAAAGACGAAGGGTCTGAC
ATGGAGAAATTGGTCGAGAAAAAAGAATGTTGCAATCCTGCCTGTGGCAGACACTT
CAGTTGTGGACGCTGATGCTCCAGGACCCTCTGAACCACGACTCGAG (SEQ ID NO:379)

Translation:
MFTVFLLVVLATTVVSFPSERASDGRDDTAKDEGSDMEKLVEKKECCNPACGRHFSCG
R (SEQ ID NO:380)

Toxin Sequence:
Xaa1-Cys-Cys-Asn-Xaa3-Ala-Cys-Gly-Arg-His-Phe-Ser-Cys-# (SEQ ID NO:381)

Name: S1.8
Species: striatus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCA
CTTCAGATCGTGCATCTGATGGCAGGGATGACGAAGCCAAAGACGAAAGGTCTGAC
ATGCACGAATCGGACCGGAAAGGACGCGCATACTGTTGCCATCCTGCCTGTGGCCC
AAACTATAGTTGTGGCACCTCATGCTCCAGGACCCTCTGAACCACGACCTCGAG
(SEQ ID NO:382)

Translation:
MFTVFLLVVLATTVVSFTSDRASDGRDDEAKDERSDMHESDRKGRAYCCHPACGPNY
SCGTSCSRTL (SEQ ID NO:383)

Toxin Sequence:
Ala-Xaa5-Cys-Cys-His-Xaa3-Ala-Cys-Gly-Xaa3-Asn-Xaa5-Ser-Cys-Gly-Thr-Ser-Cys-Ser-Arg-
Thr-Leu-^ (SEQ ID NO:384)

Name: S1.9
Species: striatus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCA
CTTCAGATCGTGCATCTGATGGCAGGGATGACGAAGCCAAAGACGAAAGGTCTGAC
ATGCACGAATCGGACCGGAAAGGACGCGCATACTGTTGCCATCCTGTCTGTGGCAA
AAACTTTGATTGTGGACGCTGATGCTCCAGGACCCTCTGAACCACGACCTCGAG
(SEQ ID NO:385)

Translation:
MFTVFLLVVLATTVVSFTSDRASDGRDDEAKDERSDMHESDRKGRAYCCHPVCGKNF
DCGR (SEQ ID NO:386)

Toxin Sequence:
Ala-Xaa5-Cys-Cys-His-Xaa3-Val-Cys-Gly-Lys-Asn-Phe-Asp-Cys-# (SEQ ID NO:387)

Name: Ra1.1
Species: rattus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCC
CTTCAGATCGTGCATCTGATGGCAGGGATGACGAAGCCAAAGACGAAAGGTCTGAC
ATGCACGAATCGGACCGGAATGGACGCGGATGCTGTTGCAATCCTGCCTGTGGCCC
AAACTATGGTTGTGGCACCTCATGCTCCAGGACCCTCTGAACCACGACCTCGAG
(SEQ ID NO:388)

Translation:
MFTVFLLVVLATTVVSFPSDRASDGRDDEAKDERSDMHESDRNGRGCCCNPACGPNY GCGTSCSRTL (SEQ ID NO:389)

Toxin Sequence:
Gly-Cys-Cys-Cys-Asn-Xaa3-Ala-Cys-Gly-Xaa3-Asn-Xaa5-Gly-Cys-Gly-Thr-Ser-Cys-Ser-Arg-Thr-Leu-^ (SEQ ID NO:390)

Name: Ar1.1
Species: arenatus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTGGATTCCTTCA CTCCAGTTCGTACTTCTGTTGGCAGGAGTGCTGCAGCCAACGCGTTTGACCGGATCG CTCTGACCGCCAGGCAAGATTATTGCTGTACCATTCCCAGCTGTTGGGATCGCTATA AAGAGAGATGTAGACACATACGCTGATGCTCCAGGACCCTCTGAACCACGACCTTG AG (SEQ ID NO:391)

Translation:
MFTVFLLVVLATTVDSFTPVRTSVGRSAAANAFDRIALTARQDYCCTIPSCWDRYKERC RHIR (SEQ ID NO:392)

Toxin Sequence:
Xaa2-Asp-Xaa5-Cys-Cys-Thr-Ile-Xaa3-Ser-Cys-Xaa4-Asp-Arg-Xaa5-Lys-Xaa1-Arg-Cys-Arg-His-Ile-Arg-^ (SEQ ID NO:393)

Name: Er1.1
Species: eburneus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTGGATTCCTTCA CTTCAGTTCGTACTTCCGTTGGCAGGAGTGCTGCAGCCAACGCGTTTGACCGGATCG CTCTGACCGCCAGGCAAGATTATTGCTGTACCATTCCCAGCTGTTGGGATCGCTATA AAGAGAGATGTAGACACATACGCTGATGCTCCAGGACCCTCTGAACCACGACCTCG AG (SEQ ID NO:394)

Translation:
MFTVFLLVVLATTVDSFTSVRTSVGRSAAANAFDRIALTARQDYCCTIPSCWDRYKERC RHIR (SEQ ID NO:395)

Toxin Sequence:

Xaa2-Asp-Xaa5-Cys-Cys-Thr-Ile-Xaa3-Ser-Cys-Xaa4-Asp-Arg-Xaa5-Lys-Xaa1-Arg-Cys-Arg-His-Ile-Arg-^ (SEQ ID NO:396)

Name: Mi1.2
Species: miles
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACTGCTGTTCTTCCAGTCA CTTTAGATCGTGCATCTGATGGAAGGAATGCAGCAGCCAACGCCAAAACGCCTCGC CTGATCGCGCCATTCATCAGGGATTATTGCTGTCATAGAGGTCCCTGTATGGTATGG TGTGGTTGAAGCCGCTGCTGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:397)

Translation:
MFTVFLLVVLATAVLPVTLDRASDGRNAAANAKTPRLIAPFIRDYCCHRGPCMVWCG (SEQ ID NO:398)

Toxin Sequence:
Asp-Xaa5-Cys-Cys-His-Arg-Gly-Xaa3-Cys-Met-Val-Xaa4-Cys-# (SEQ ID NO:399)

Name: Jp1.1
Species: jaspedius
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCAACT CTTCAGATCGTGGTCCAGCATCTAATAAAAGGAAGAATGCCGCAATGCTTGACATG ATCGCTCAACACGCCATAAGGGGTTGCTGTTCCGATCCTCGCTGTAGATATAGATGT CGTTGAAGACGCTGCTGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:400)

Translation:
MFTVFLLVVLATTVVSNSSDRGPASNKRKNAAMLDMIAQHAIRGCCSDPRCRYRCR (SEQ ID NO:401)

Toxin Sequence:
Gly-Cys-Cys-Ser-Asp-Xaa3-Arg-Cys-Arg-Xaa5-Arg-Cys-Arg-^ (SEQ ID NO:402)

Name: a-OmIA
Species: omaria
Isolated: Yes

Toxin Sequence:

Gly-Cys-Cys-Ser-His-Xaa3-Ala-Cys-Asn-Val-Asn-Asn-Xaa3-His-Ile-Cys-Gly-# (SEQ ID NO:403)

Name: a-OmIA [COOH]
Species: omaria
Cloned: No

Toxin Sequence:
Gly-Cys-Cys-Ser-His-Xaa3-Ala-Cys-Asn-Val-Asn-Asn-Xaa3-His-Ile-Cys-Gly-^ (SEQ ID NO:404)

Name: Qc1.1
Species: quercinus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCACTTCAGATC GTGTATCTAATGGCAGGAAAGCTGCAGCCAAATTCAAAGCGCCTGCCCTGATGGAG CTGTCCGTCAGGCAAGGATGCTGTTCAGATCCTGCCTGTGCCGTGAGCAATCCAGAC ATCTGTGGCGGAGGACGCTGATGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:405)

Translation:
MFTVFLLVVLATTVTSDRVSNGRKAAAKFKAPALMELSVRQGCCSDPACAVSNPDICG GGR (SEQ ID NO:406)

Toxin Sequence:
Xaa2-Gly-Cys-Cys-Ser-Asp-Xaa3-Ala-Cys-Ala-Val-Ser-Asn-Xaa3-Asp-Ile-Cys-Gly-Gly-# (SEQ ID NO:407)

Name: Bn1.6
Species: bandanus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTTGTTTCCTTCA CTTCAAATCGTGCATTTCGTCGTAGGAATGCCGTAGCCAAAGCGTCTGACCTGATCG CTCTGAACGCCAGGAGACCAGAATGCTGTACTCATCCTGCCTGTCACGTGAGTCATC CAGAACTCTGTGGTTGAAGACGCTGACGCTCCAGGACCCTCTGAACCACGACCTCG AG (SEQ ID NO:408)

Translation:
MFTVFLLVVLATTVVSFTSNRAFRRRNAVAKASDLIALNARRPECCTHPACHVSHPELC G (SEQ ID NO:409)

Toxin Sequence:
Xaa3-Xaa1-Cys-Cys-Thr-His-Xaa3-Ala-Cys-His-Val-Ser-His-Xaa3-Xaa1-Leu-Cys-# (SEQ ID NO:410)

Name: Mr1.5
Species: marmoreus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTTGTTTCCTTCA
CTTCAAATCGTGTTCTGGATCCAGCATTTCGTCGTAGGAATGCCGCAGCCAAAGCGT
CTGACCTGATCGCTCTGAACGCCAGGAGACCAGAATGCTGTACTCATCCTGCCTGTC
ACGTGAGTAATCCAGAACTCTGTGGCTGAAGACGCTGATGCTCCAGGACCCTCTGA
ACCACGACCTCGAG (SEQ ID NO:411)

Translation:
MFTVFLLVVLATTVVSFTSNRVLDPAFRRRNAAAKASDLIALNARRPECCTHPACHVSN
PELCG (SEQ ID NO:412)

Toxin Sequence:
Xaa3-Xaa1-Cys-Cys-Thr-His-Xaa3-Ala-Cys-His-Val-Ser-Asn-Xaa3-Xaa1-Leu-Cys-# (SEQ ID NO:413)

Name: Mi1.1
Species: miles
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCGTCA
CTTCATATCGTGCATCTCATGGCAGGAAGGACGCAGCCGACCTGAGCGCTCTGAAC
GACAACAATAATTGCTGTAACCATCCTGCCTGTGCCGGGAAAAATTCAGATCTTTGT
GGTTGAAGACGCTGCTGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:414)

Translation:
MFTVFLLVVLATTVVSVTSYRASHGRKDAADLSALNDNNNCCNHPACAGKNSDLCG
(SEQ ID NO:415)

Toxin Sequence:
Cys-Cys-Asn-His-Xaa3-Ala-Cys-Ala-Gly-Lys-Asn-Ser-Asp-Leu-Cys-# (SEQ ID NO:416)

Name: MII[YHT]
Species: magus

Toxin Sequence:
Gly-Cys-Cys-Xaa5-His-Xaa3-Thr-Cys-His-Leu-Xaa1-His-Ser-Asn-Leu-Cys-# (SEQ ID NO:417)

Name: Nb1.1
Species: nobilis
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTTGTTTCCTTCA
CTTCAGATCGTGCATCTGATGGCAGGAATGCCGCAGCCAAAGCTTCTGACCTGATTG
CTTTGACCGTCAGGGGATGCTGTGAGCGACCTCCCTGTCGCTGGCAAAATCCAGATC
TTTGTGGTGGAAGGCGCTGANATTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:418)

Translation:
MFTVFLLVVLATTVVSFTSDRASDGRNAAAKASDLIALTVRGCCERPPCRWQNPDLCG GRR (SEQ ID NO:419)

Toxin Sequence:
Gly-Cys-Cys-Xaa1-Arg-Xaa3-Xaa3-Cys-Arg-Xaa4-Gln-Asn-Xaa3-Asp-Leu-Cys-Gly-# (SEQ ID NO:420)

Name: Ak1.1
Species: atlanticus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACAGTCGTTTCCTTCA
CTTCAGATAGTGCATTTGATAGCAGGAATGTCGCAGCCAACGACAAAGTGTCTGAC
ATGATCGCTCTGACCGCCAGGAGAACATGCTGTTCCCGTCCTACCTGTAGAATGGAA
TATCCAGAACTTTGTGGTGGAAGACGCTGATACTCCAGGACCCTCTGAACCACGAC
CTCGAG (SEQ ID NO:421)

Translation:
MFTVFLLVVLATTVVSFTSDSAFDSRNVAANDKVSDMIALTARRTCCSRPTCRMEYPEL CGGRR (SEQ ID NO:422)

Toxin Sequence:
Thr-Cys-Cys-Ser-Arg-Xaa3-Thr-Cys-Arg-Met-Xaa1-Xaa5-Xaa3-Xaa1-Leu-Cys-Gly-# (SEQ ID NO:423)

Name: Qc1.2

Species: quercinus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAATCACGGTGGTTTCCTTCA
CCTCAGATCATGCATCTGATGGCAGGAATACCGCAGCCAACGACAAAGCGTCTAAA
CTGATGGCTCTTACGAACGAATGCTGTGACAATCCTCCGTGCAAGTCGAGTAATCCA
GATTTGTGTGACTGGAGAAGCTGATGCTCCAGGACCCTNTGAACCACGACCTCGAG
(SEQ ID NO:424)

Translation:
MFTVFLLVVLAITVVSFTSDHASDGRNTAANDKASKLMALTNECCDNPPCKSSNPDLC
DWRS (SEQ ID NO:425)

Toxin Sequence:
Asn-Xaa1-Cys-Cys-Asp-Asn-Xaa3-Xaa3-Cys-Lys-Ser-Ser-Asn-Xaa3-Asp-Leu-Cys-Asp-Xaa4-
Arg-Ser-^ (SEQ ID NO:426)

Name: Lp1.1
Species: leopardus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACGGTCGTTTCCCTCA
CTTTAGATCGTGCATCTGGTGGCAGGAGATCTGGAGCCGACAACATGATTGCTCTTC
TGATCATCAGAAAATGCTGTTCCAATCCCGCCTGTAACAGGTATAATCCAGCAATTT
GTGATTGAAGACGCTAATGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID
NO:427)

Translation:
MFTVFLLVVLATTVVSLTLDRASGGRRSGADNMIALLIIRKCCSNPACNRYNPAICD
(SEQ ID NO:428)

Toxin Sequence:
Cys-Cys-Ser-Asn-Xaa3-Ala-Cys-Asn-Arg-Xaa5-Asn-Xaa3-Ala-Ile-Cys-Asp-^ (SEQ ID
NO:429)

Name: Em1.1
Species: emaciatus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTCTCTTGGCAACCACTGTCACTTTACATC
GTGCATCTAATGGCAGGAATGCCGCAGCCAGCAGGAAAGCGTCTGCCCTGATCGCT
CAGATCGCCGGTAGAGACTGCTGTAACTTTCCTGCTTGTGCCGCGAGTAATCCAGGC

CTTTGTACTTGAAGACGCTGCTGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:430)

Translation:
MFTVFLLVLLATTVTLHRASNGRNAAASRKASALIAQIAGRDCCNFPACAASNPGLCT (SEQ ID NO:431)

Toxin Sequence:
Asp-Cys-Cys-Asn-Phe-Xaa3-Ala-Cys-Ala-Ala-Ser-Asn-Xaa3-Gly-Leu-Cys-Thr-^ (SEQ ID NO:432)

Name: C. victor alpha
Species: victor
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACCATCGTTTCCTCCA
CTTTAGATCGTGCATCTGATGGCATGAATGCTGCAGCGTCTGACCTGATCGCTCTGA
GCATCAGGAGATGCTGTTCTTCTCCTCCCTGTTTCGCGAGTAATCCAGCTTGTGGTA
GACGACGCTGATGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:433)

Translation:
MFTVFLLVVLATTIVSSTLDRASDGMNAAASDLIALSIRRCCSSPPCFASNPACGRRR (SEQ ID NO:434)

Toxin Sequence:
Cys-Cys-Ser-Ser-Xaa3-Xaa3-Cys-Phe-Ala-Ser-Asn-Xaa3-Ala-Cys-# (SEQ ID NO:435)

Name: Cj1.1
Species: cinereus gubba
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCCTGGCAACCACTATCGTTTCCTCCA
CTTCAGGTCATGCATTTGATGGCAGGAATGCTGCAGCCGACTACAAAGGGTCTGAA
TTGCTTGCTATGACCGTCAGGGGAGGATGCTGTTCCTTTCCTCCCTGTATCGCAAAT
AATCCTTTTTGTGCTGGAAGACGCTGATGCTCCAGGACCCTCTGAACCACGACCTCG
AG (SEQ ID NO:436)

Translation:
MFTVFLLVVLATTIVSSTSGHAFDGRNAAADYKGSELLAMTVRGGCCSFPPCIANNPFC
AGRR (SEQ ID NO:437)

Toxin Sequence:

Gly-Gly-Cys-Cys-Ser-Phe-Xaa3-Xaa3-Cys-Ile-Ala-Asn-Asn-Xaa3-Phe-Cys-Ala-# (SEQ ID NO:438)

Name: Fd1.1
Species: flavidus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTCGCATCCTCTGTCACTTTAGATC
GTGCATCTCATGGCAGGTATATCCCAGTCGTCGACAGAGCGTCTGCCCTGATGGCTC
AGGCCGACCTTAGAGGTTGCTGTTCCAATCCTCCTTGTTCCTATCTTAATCCAGCCTG
TGGTTAAAGACGCTGCCGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:439)

Translation:
MFTVFLLVVFASSVTLDRASHGRYIPVVDRASALMAQADLRGCCSNPPCSYLNPACG (SEQ ID NO:440)

Toxin Sequence:
Gly-Cys-Cys-Ser-Asn-Xaa3-Xaa3-Cys-Ser-Xaa5-Leu-Asn-Xaa3-Ala-Cys-# (SEQ ID NO:441)

Name: Em1.2
Species: emaciatus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTCGCATCCTCTGTCACTTTAGATC
GTGCATCTCATGGCAGGTATGCCGCAGTCGTCAACAGAGCGTCTGCCCTGATGGCTC
ATGCCGCCCTTCGAGATTGCTGTTCCGATCCTCCTTGTGCTCATAATAATCCAGACT
GTCGTTAAAGACGCTGCTGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:442)

Translation:
MFTVFLLVVFASSVTLDRASHGRYAAVVNRASALMAHAALRDCCSDPPCAHNNPDCR (SEQ ID NO:443)

Toxin Sequence:
Asp-Cys-Cys-Ser-Asp-Xaa3-Xaa3-Cys-Ala-His-Asn-Asn-Xaa3-Asp-Cys-Arg-^ (SEQ ID NO:444)

Name: Ge1.1
Species: generalis
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACTACTGTCGTTTCCTTCA
CTTCAGATCGTGGGTCTGATGGCAGGAATGCCGCAGCCAAGGACAAAGCGTCTGAC
CTGGTCGCTCTGACCGTCAAGGGATGCTGTTCTAATCCTCCCTGTTACGCGAATAAT
CAAGCCTATTGTAATGGAAGACGCTGATGCTCCAGGACCCTCTGAACCACGACCTC
GAG (SEQ ID NO:445)

Translation:
MFTVFLLVVLATTVVSFTSDRGSDGRNAAAKDKASDLVALTVKGCCSNPPCYANNQA
YCNGRR (SEQ ID NO:446)

Toxin Sequence:
Gly-Cys-Cys-Ser-Asn-Xaa3-Xaa3-Cys-Xaa5-Ala-Asn-Asn-Gln-Ala-Xaa5-Cys-Asn-# (SEQ ID NO:447)

Name: Wi1.1
Species: wittigi
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCCTGGCAACCACTGTCGTTTCCCCCA
CTAGAGATCGTGCATCTGGTGTCAGGAATGTTGTTGCAACAAGCTTTCAGACTCTGA
CCCACGATGAATGCTGTGCACACCCTTCCTGTTGGAAGGCCGAAGACCTGATTTGTA
CTAATCAACGTCGCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:448)

Translation:
MFTVFLLVVLATTVVSPTRDRASGVRNVVATSFQTLTHDECCAHPSCWKAEDLICTNQ
RRRTL (SEQ ID NO:449)

Toxin Sequence:
Asp-Xaa1-Cys-Cys-Ala-His-Xaa3-Ser-Cys-Xaa4-Lys-Ala-Xaa1-Asp-Leu-Ile-Cys-Thr-Asn-Gln-Arg-Arg-Arg-Thr-Leu-^ (SEQ ID NO:450)

Name: Ca1.5
Species: caracteristicus
Cloned: Yes

DNA Sequence:
GGATCCATGTTCACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCA
CTTCAGATCGTGCGTCTGAAGGCAGGAATGCTGCAGCCAAGGACAAAGCGTCTGAC
CTGGTGGCTCTGAGAGTCAGGGGATGCTGTGCCATTCGTGAATGTCGCTTGCAGAAT
GCAGCGTATTGTGGTGGAATATCCTGATGCTCCAGGACCCTCTGAACCACGACCTCG
AG (SEQ ID NO:451)

Translation:
MFTVFLLVVLATTVVSFTSDRASEGRNAAAKDKASDLVALRVRGCCAIRECRLQNAAY
CGGIS (SEQ ID NO:452)

Toxin Sequence:
Gly-Cys-Cys-Ala-Ile-Arg-Xaa1-Cys-Arg-Leu-Gln-Asn-Ala-Ala-Xaa5-Cys-Gly-Gly-Ile-Ser-^
(SEQ ID NO:453)

Name: Bt1.10
Species: betulinus
Cloned: Yes

DNA Sequence:
AGTAATTNATATANNAGAAAGNAANANAAAANNATANAGAATTTAAGTAATNTAA
GAANNGAGANAGTGAATAGNAGNTAAGTAGANNAAGANAGGTAGANAGNANANG
NGGANGNTAGNTAATAGATANNNTATNGAGANATTANTAGCNGTATANANAAGAA
AAGAGGGNAANNGAAATGNNGNAANNATAANTANTANNGATNGANNNGNAAGTG
NNAAGNGTANAAGGAANAACAAANTNGTTGTNTAATNTGNNTGNGTGTGTNTGTGT
GNGTGTGTGTGTGTGNGTGNGTGTGTNTGTGNGNNTGTGTGNGNGNGNGNGTGTGT
GTGTGNGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGNGTGTGTGGTTCTGGA
TCCAGCATCTGGTGGCAGGAAGGCTGCAGCCAAAGCGTCTAACCGGATCGCTCTGA
CCGTCAGGAGTGCAACATGCTGTTATTATCCTCCCTGTTACGAGGCTTATCCAGAAA
GTTGTCTGTAACGTGAATCATCCAGACCTTTGTGGCTGAAGACCCTGATGCTCCAGG
GGCAAGTTCAA (SEQ ID NO:454)

Translation:
SGGRKAAAKASNRIALTVRSATCCYYPPCYEAYPESCL (SEQ ID NO:455)

Toxin Sequence:
Ser-Ala-Thr-Cys-Cys-Xaa5-Xaa5-Xaa3-Xaa3-Cys-Xaa5-Xaa1-Ala-Xaa5-Xaa3-Xaa1-Ser-Cys-
Leu-^ (SEQ ID NO:456)

Where:
Xaa1 is Glu or γ-carboxy-Glu
Xaa2 is Gln or pyro-Glu
Xaa3 is Pro or hydroxy-Pro
Xaa4 is Trp (D or L) or bromo-Trp (D or L)
Xaa5 is Tyr, ^{125}I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
^ is free carboxyl or amidated C-terminus, preferably free carboxyl
# is free carboxyl or amidated C-terminus, preferably amidated
? is free carboxyl or amidated C-terminus

TABLE 2

Alignment of γ-Conopeptides[1] (SEQ ID NO:)

4/43 SNX	-------DCRGYDAPCSSGAPCCDWWTCSARTNRCF^	(457)
Af6.1	GMW---GDCKDGLTTCFAPSECCSE-DC-E-GS-CTMW^	(458)
Af6.2	---WREGSCTSWLATCTQDQQCCTD-VCYKRDY-CALWDDR^	(459)
Af6.3	----N---CSDDWQYCESPSDCCSW-DC-D-VV-CS#	(460)
Af6.4	--WWRWGGCMAWFGKCSKDSECCSN-SC-DITR-CELMRFPPDW^	(461)
Af6.5	-------DCRGYDAPCSSGAPCCDWWTCSARTGRCF^	(462)
Af6.6	---L----CPDYTEPCSHAHECCSW-NC-HNGH-CT#	(463)
Af6.7	--------CSSWAKYCEVDSECCSE-QC-VRSY-CAMW^	(464)
g-PnVIIA	-------DCTSWFGRCTVNSXCCSN-SC-DQTY-CXLYAFOS^[2]	(465)
Gm6.7	-------ECRAWYAPCSPGAQCCSLLMCSKATSRCILAL^[2]	(466)
J010	--------CKTYSKYCXADSXCCTX-QC-VRSY-CTLF#[2]	(467)
Mr6.1	----N-GQCEDVWMPCTSNWXCCSL-DC-E-MY-CTQI#[2]	(468)
Mr6.2	--------CGGWSTYCEVDEXCCSE-SC-VRSY-CTLF#[2]	(469)
Mr6.3	----N-GGCKATWMSCSSGWXCCSM-SC-D-MY-C#[2]	(470)
R6.10	--UFGHXXCTYULGPCXVDDTCCSA-SC-XSKF-CGLU^	(471)
R6.9	--WWE-GECSNWLGSCSTPSNCCLK-SC-N-GH-CTLW^	(472)
Tx6.1	---L----CODYTXOCSHAHXCCSW-NC-YNGH-CT#[2]	(473)
Tx6.14	-------DCYSWLGSCIAPSQCCSE-VC-D-YY-CRLWR^	(474)
Tx6.4	--WL---ECSVWFSHCTKDSXCCSN-SC-DQTY-CTLMPPDW^[2]	(475)
Tx6.5	GMW---GECKDGLTTCLAPSXCCSE-DC-E-GS-CTMW^[2]	(476)
Tx6.6	D-WWD-DGCSV-WGPCTVNAXCCSG-DC-H-ET-CIFGWEV^[2]	(477)
Tx6.9	--WWRWGGCMAWFGLCSRDSXCCSN-SC-DVTR-CELMPFPPDW^[2]	(478)
TxVIIA	--------CGGYSTYCXVDSXCCSD-NC-VRSY-CTLF#	(479)

[1] The E may be Glu or Gla, the P may be Pro or hydroxy-Pro, and W may be Trp or bromo-Trp.
[2] Peptide disclosed in U.S. Serial No. 09/210,952 (PCT/US98/26792).

TABLE 3

Alignment of σ-Conopeptides (SEQ ID NO:)

Ca8.1	GCS-GT-CHRREDGKC-RGTCDCSG-YSYCRCG-DAHHFYRGCTCSCQ#	(480)
Ca8.2	GCSG-T-CHRREDGKC-RGTCDCSG-YSYCRCG-DAHHFYRGCTCTC^	(481)
Ca8.3	GCSG-T-CRRHRDGKC-RGTCDCSG-YSYCRCG-DAHHFYRGCTCTC^	(482)
Ca8.4	GCSG-T-CRRHRDGKC-RGTCDCSG-YSYCRCG-DAHHFYRGCTCTC^	(483)
Ca8.5	GCSG-T-CHRREDGKC-RGTCDCSG-YSYCRCG-DAHHFYRGCTCTC^	(484)
Ca8.6	GCSG-T-CHRRQNGEC-QGTCDCDG-HDHCDCG-DTLGTYSGCVCIC^	(485)
La8.1	QSE--TACRSLGSYQCM-GKCQ-LGVHSWCECIYNRGSQKSGCACRCQK^	(486)
Mn8.1	QCTLVNNCDRNGERACN-GDCSCEGQI--CKCGYRVSPGKSGCACTCRNAK^	(487)
P8.1	GCS-GSPCFKNKT--C-RDECICGG-LSNCWCGY-GGS--RGCKCTCRE^	(488)
R8.1	KCNF-DKCKGTGVYNCG-ESCSCEGLHS-CRCTYNIGSMKSGCACICTYY^	(489)
R8.2	YGLGCA-GT-CGSSSN--CVRDYCDC-P-KPNCYCT-GKGFRQPGCGCSCL#	(490)
Sx8.1	QCTFVNNCQQNG--CAN-GDCSCGDQI--CKCGYRISPGRSGCACTCRNAK^	(491)
T8.1	FGPIC---T-CFKSQN--C-RGSCECMS-PPGCYCS-NNGIRERGCSCTCPGT#	(492)
T8.2	GCT--GNCDW----TCS-GDCSCQGTSDSCHCIPPKSIGNR-CRCQCKRKIEID^	(493)

TABLE 4

Alignment of τ-Conopeptides (SEQ ID NO:)

	Tx5.2a	---ECCEDGW-CCTAAPLT#[1] (494)
	Tx5.2b	---GCCEDGW-CCTAAPLT#[1] (495)
5	Mr5.1	--NGCC-RAGDCCSRFEIKENDF#[1] (496)
	Mr5.3	--NGCC-RAGDCCS^[1] (497)
	Mr5.2	--NACC-IVRQCC^[1] (498)
	Qc5.1	---GCCAR-LTCCV#[1] (499)
	Qc5.2	---GCCAM-LTCCV#[1] (500)
10	t-PVA	---GCCPKQMRCCTL#[1] (501)
	Ca5.1	----CCPRRLACCII#[1] (502)
	Ca5.2	----CCPNK-PCCFI#[1] (503)
	G5.1	-ZGWCCKENIACCI^[1] (504)
	G5.2	-ZGWCCKENIACCV^[1] (505)
15	Im5.1	DWNSCCGKNPGCCPW#[1] (506)
	Bt5.1	---NCCPDSPPCCH^ (507)
	Af5.2	--GNCCEFWEFCCD^ (508)
	Da5.1	----CCEYWKLCC# (509)
	Om5.1	---VCCGYKFFCCR^ (510)
20	t-AuVA	---FCCPVIRYCCW^[1] (511)
	t-AuVB	---FCCPFIRYCCW^[1] (512)
	Au5.1	----CCPMIYWCCS^ (513)
	Au5.4	----CCPEIYWCCS^ (514)
	Nb5.1	---ICCPIILWCC# (515)
25	Af5.1	----CCPPVIWCC# (516)
	Tx5.1	----CCQTFYWCCVQ#[1] (517)
	Au5.3	WNNYCCTNELWCC# (518)
	Gm5.1	---LCCVTEDWCCEWW^[1] (519)
	Gm5.2	---VCCRPVQDCCS#[1] (520)
30	Da5.2	-PVNCCPIDQSCCS^ (521)
	Sf5.1	GNIHCCTKYQPCCSSPS^ (522)

[1] Peptide disclosed in U.S. Serial No. 09/497,491 (PCT/US00/03021).

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TABLE 5

Alignment of Mar-Type Conopeptides[1] (SEQ ID NO:)

	Tx1.6 (Q819)	-ZTCCGYRMCVPC# (523)
	Bn1.5 (Q818)	-A-CCGYKLCSPC^ (524)
	Pn1.3 (Q820)	-STCCGFKMCIPCR^ (525)
40	Pn1.5 (AA200)	-STCCGFKMCIPCS^ (526)
	Pn1.7 (AA456)	-STCCGFKMCIPC# (527)
	Ep1.5 (AA457)	-STCCGYRMCVPC# (528)
	Mr1.3	NGVCCGYKLCLPC^ (529)
	Pn1.6 (AA390)	--LCCGFWMCIPCN^ (530)
45	Mr1.1	NGVCCGYKLCHOC^ (531)

Mr1.2	-GVCCGYKLCHOC^ (532)
Bn1.5	--ACCGYKLCSPC^ (533)
Au1.4	-SVCCGYKLCFPC# (534)
Tx1.7	NGVCCGYRMCVPC# (535)
Tx1.6	-ZTCCGYRMCVPC# (536)
Af1.3	-ZACCGFKMCVPC# (537)
Pn1.3	-STCCGFKMCIPCR^ (538)
Pn1.4	NGVCCGFWMCIPCN^ (539)
Om1.7	-DVCCYVRMC-PCR^ (540)

[1] Some peptides disclosed in U.S. Serial No. 09/580,201. P may also be O and O may also be P.

TABLE 6

Alignment of Contryphans* (SEQ ID NO:)

Contryphan-Im	Z--C-GQAWC# (541)
Contryphan-Sm-dW4, V7	GCOWQPVC# (542)
Contryphan-Ar-1	ZYGCOOGLWCH^ (543)
C. arenatus contryphan 1A	ASGCPWRPWC# (544)
C. arenatus contryphan 2	ZYGCPVGLWCD^ (545)
C. arenatus contryphan 4	SGCPWQPWC# (546)
C. arenatus contryphan 1	SGCPWHPWC# (547)

* P may be Pro or hydroxy-Pro; Z may be Gln or pyro-Glu.

TABLE 7

Alignment of αA-Conopeptides* (SEQ ID NO:)

αA-EIVB	GCCGKYONAACHOCGCTVGROOYCDROSGG# (548)
P4.1	GCCGSYPNAACHPCGCK-DRPSYCGQ# (549)
P4.2	EGCC---SNPACHPCGCK-DRPSYCGQ# (550)

* P may be Pro or hydroxy-Pro

TABLE 8

Alignment of Bromosleeper Conopeptides* (SEQ ID NO:)

Bromosleeper-Ar1	VVTEACEESCEEEEKHCCHVNNGVPSCAVICW# (551)
Bromosleeper-Ar1A	IVTEACEESCEDEEKHCCHVNNGVPSCAVICW# (552)
Bromosleeper-Ar2	IVTEACEEHCEDEEQFCCGLENGQPFCAPVCF# (553)
Bromosleeper-Ar3	VVTGACEEHCEDEEKHCCGLENGQPFCARLCL# (554)
Bromosleeper-Di1	NVDQECIDACQLEDKNCCGRTDGEPRCAKICL# (555)
Bromosleeper-Di2	ETDQECIDICKQEDKKCCGRSNGEPTCAKICL# (556)
Bromosleeper-Di3	ETDQECIDTCEQEDKKCCGRTNGEPVCAKICF# (557)
Bromosleeper-P1	PKTEACEEVCELEEKHCCCIRSDGPKCSRKCLLSIFC^ (558)
Bromosleeper-P2	VVSEECKKYCKKQNKNCCSSKHEEPRCAKICF# (559)
Bromosleeper-Sn	AVTEACTEDCKTQDKKCCGEMNGQHTCAKICL# (560)

Bromosleeper-T1 PKTKE**C**ERY**C**ELEEKH**CCC**IRSNGPK**C**SRI**C**IFKFW**C**^ (561)
Bromosleeper-T2 PKTRE**C**EMQ**C**EQEEKH**CC**RVRDGTGQ**C**APK**C**LGINW^ (562)

* The E may be Glu or Gla, the P may be Pro or hydroxy-Pro, and W may be Trp or bromo-Trp.

TABLE 9

Alignment of Conopressins (SEQ ID NO:)

Conopressin-G **C**FIRN**C**PKG# (563)
Conopressin-S **C**IIRN**C**PRG# (564)

TABLE 10

Alignment of O-Superfamily (SEQ ID NO:)

Ar6.1 -----G**C**TPPGGV**C**GYHGH---**CC**D-F-**C**---DTFGNL**C**VS# (565)
C. geogr. GS-A -----A**C**SGRGSR**C**PPQ-----**CC**MGLT**C**--GREYPPR**C**# (566)
Ca6.3 (F166) -----N**C**GEQGEG**C**AT--RP--**CC**SGLS**C**-VGSRPGGL**C**QY# (567)
convulsion -----N**C**PY----**C**VVY-----**CC**PPAY**C**EASG-----**C**RPP# (568)
De6.1 -----A**C**KOKNNL**C**AITXMAX-**CC**SGF-**C**LIY-----R**C**^ (569)
Lv6.2 (I16) -----S**C**GHSGAG**C**YT--RP--**CC**PGLH**C**-SGGQAGGL**C**V^ (570)
Lv6.3 (I12) -----D**C**GESGQG**C**YSV-RP--**CC**PGLI**C**KGTG-GGGL**C**RPSGI^ (571)
Mf6.1 (F204) ------**C**TPPGGL**C**-YHAYP--**CC**SKT-**C**---NLDTSQ**C**EPRWS^ (572)
Mi6.2 (F162) ------**C**TDDSQF**C**NPSNHD--**CC**SG-K**C**IDEGDNG-I**C**AIVPENS^ (573)
Mi6.3 (F161) ------**C**TEDSQF**C**NPSNHD--**CC**SG-K**C**IDEGDNG-I**C**AIVPENS^ (574)
Pu6.1 (JG14) ------**C**SDFGSD**C**VPATHN--**CC**SG-EC**F**GFEDFG-L**C**T^ (575)
Qc6.4 (F025) -----A**C**SQVGEA**C**FPQ-KP--**CC**PGFL**C**--NH-IGGM**C**HH^ (576)
S6.4 ------**C**LPDGTS**C**LFSRIR--**CC**GT--**C**---SSILKS**C**VS^ (577)
Ts6.3 (F081) -----S**C**AEFGEV**C**-SS-TA--**CC**PDLD**C**VEAYSP--I**C**LWE^ (578)
Tx6.3 -----K**C**VEQWKY**C**TR---ESL**CC**AGL-**C**LFS-----F**C**IL^ (579)
Tx6.7 ------**C**VEQWEV**C**GIILFSSS**CC**GQL-**C**LFG-----F**C**VL^ (580)
Vr6.1 (F198) -----D**C**GGQGEG**C**YT--QP--**CC**PGLR**C**RGGGTGGGV**C**QL^ (581)
Wi6.1 (M406) FGSFIP**C**ARLGEP**C**-----T-I**CC**RPLR**C**RESG--TPT**C**QV^ (582)
Rg6.6 (K861) -----T**C**LEHNKL**C**WYD---RD**CC**TIY-**C**---N--ENK**C**GVKPQ^ (583)

EST202 -----A**C**KSNYD**C**PQRFK**CC**SYTWNGSSGY**C**KRV**C**YLYR^ (584)

TABLE 11

Alignment of ψ-Conopeptides* (SEQ ID NO:)

ψ-PIIIF GOOCCLYGSCROFOGCYNALCCRK# (585)
U021 homolog HPPCCMYGRCRRYPGCSSASCCQG# (586)

* P may be Pro or hydroxy-Pro

TABLE 12

Alignment of kappaA-Conopeptides* (SEQ ID NO:)

Cn10.3 (J454) APELVVTATTT**CC**GYDPMTI**C**PP**C**M**C**THS**C**PPKRKP# (587)
A10.2 (H350) ZSWLVPSTITT**CC**GYDPGTM**C**PP**C**R**C**NNT**C**KPKKPKPGK# (588)

Cn10.4 (G851)	APELVVTATTTCCGYDPMTWCPSCMCTYSCPHQRKKP# (589)
M10.3 (X003)	APELVVTATTTCCGYDPMTICPPCMCTHSCPPKGKP# (590)
A10.3 (AA400)	ZKWLVHSKITYCCGYNKMDMCPPCMCTYSCPPLKKKRP# (591)
A10.4 (AA401)	APWTVVTATTNCCGITGPG-CLPCRCTQTC# (592)

TABLE 13

Alignment of α-Conopeptides (SEQ ID NO:)

G1.4	-ECCHPACGKHYSC# (593)
G1.5	-ECCNPACGRHFSC# (594)
S1.8	AYCCHPACGPNYSCGTSCSRTL^ (595)
S1.9	AYCCHPVCGKNFDC# (596)
Ra1.1	GCCCNPACGPNYGCGTSCSRTL^ (597)
Ar1.1	ZDYCCTIPSCWDRYKERCRHIR^ (598)
Er1.1	ZDYCCTIPSCWDRYKERCRHIR^ (599)
Mi1.2	-DYCCHRGPCMVW----C# (600)
Jp1.1	--GCCSDPRC--RYR--CR^ (601)
a-OmIA	--GCCSHPACNVNNPHICG# (602)
a-OmIA [COOH]	--GCCSHPACNVNNPHICG^ (603)
Qc1.1	Z-GCCSDPACAVSNPDICGG# (604)
Bn1.6	PE-CCTHPACHVSHPELC# (605)
Mr1.5	PE-CCTHPACHVSNPELC# (606)
Mi1.1	---CCNHPACAGKNSDLC# (607)
MII[YHT]	--GCCYHPTCHLEHSNLC# (608)
Nb1.1	--GCCERPPCRWQNPDLCG# (609)
Ak1.1	--TCCSRPTCRMEYPELCG# (610)
Qc1.2	NE-CCDNPPCKSSNPDLCDWRS^ (611)
Lp1.1	---CCSNPACNRYNPAICD^ (612)
Em1.1	-D-CCNFPACAASNPGLCT^ (613)
C. victor alpha	---CCSSPPCFASNPA-C# (614)
Cj1.1	-GGCCSFPPCIANNPF-CA# (615)
Fd1.1	--GCCSNPPCSYLNPA-C# (616)
Em1.2	-D-CCSDPPCAHNNPD-CR^ (617)
Ge1.1	--GCCSNPPCYANNQAYCN# (618
Wi1.1	DE-CCAHPSCWKAEDLICTNQRRRTL^ (619)
Ca1.5	--GCCAIRECRLQNAAYCGGIS^ (620)
Bt1.10	SATCCYYPPCYEAYPESCL^ (621)

TABLE 14

Alignment of Conopeptides* (SEQ ID NO:)

Convulsant	VYXTHP^ (622)
WG002	WSWRMGNGDRRSDQ^ (623)
QcII	DCQPCGHNVCC^ (624)
Scratching, Convulsion	KFLSGGFKXIVCHRYCAKGIAKEFCNCPD# (625)
MAG-1	RPKNSW^ (626)

MAG-2	AROKNSW? (627)
MAG-3	ROKNSW^ (628)
EST66	CCPSSKEDSLNCIETMATTATCMKSNKGEIYSYACGYCGKKKESCFG DKKPVTDYQCQTRNIPNPCGGAAL^ (629)
G12.2	DESKCDRCNCAELRSSRCTQAIFCLTPELCTPSISCPTGECRCTKFH QSRCTRFVECVPNKCRDA^ (630)
G12.1	DDSYCDGCLCTILKKETCTSTMSCRGT-- CRKEWPCWEEDCYCTEIQG GACVTPSECKPGEC^ (631)
EST171	GCVYEGIEYSVGETYQADCNTCRCDGFDLATCTVAGCTGFGPE^ (632)
U010 homolog	SGPADCCRMKECCTDRVNECLQRYSGREDKFVSFCYQEATVTCGSFN EIVGCCYGYQMCMIRVVKPNSLSGAHEACKTVSCGNPCA^ (633)
P29	DCCGVKLEMCHPCLCDNSCKNYGK# (634)
EST87	GEPIPTTVINYGECCKDPSCWVKVKDFQCPGASPPN^ (635)
Ge3.1 (F590)	QCCTFCNFGCQPCCVP^ (636)
Ts10.1	DGCPPHPVPGMHKCMCTNTC (637)
Conophysin-R	HPTKPCMYCSFGQCVGPHICCGPTGCEMGTAEANMCSEEDEDPIPCQV FGSDCALNNPDNIHGHCVADGICCVDDTCTTHLGCL^ (638)

* Conopeptides grouped together are homologous.

[0080] It will be appreciated that the methods and compositions of the instant invention can be incorporated in the form of a variety of embodiments, only a few of which are disclosed herein. It will be apparent to the artisan that other embodiments exist and do not depart from the spirit of the invention. Thus, the described embodiments are illustrative and should not be construed as restrictive.

LIST OF REFERENCES

Abiko, H. et al. (1986). *Brain Res.* **38**:328-335.

Aldrete, J.A. et al. (1979). *Crit. Care Med.* **7**:466-470.

Barnay, G. et al. (2000). *J. Med. Chem.*

Bitan, G. et al. (1997). *J. Peptide Res.* **49**:421-426.

Bodansky et al. (1966). *Chem. Ind.* **38**:1597-98.

Bulbring, W. and Wajda, J. (1945). *J. Pharmacol. Exp. Ther.* **85**:78-84.

Cartier, G.E. et al. (1996). *J. Biol. Chem.* **271**:7522-7528.

Chandler, P. et al. (1993). *J. Biol. Chem.* **268**:17173-17178.

Chaplan S.R. (1994). *J Neuroscience Methods* **53**:55-63.

Chaplan S.R. (1997). *J Pharmacol. Exp. Ther.* **280**:829-838.

Clark, C. et al. (1981). *Toxicon* **19**:691-699.

Codere, T.J. (1993). *Eur. J. Neurosci.* **5**:390-393.

Craig, A.G. et al. (1997). *J. Biol. Chem* **272**:4689-4698.

Craik, D.J. et al. (2001). *Toxicon* **39**:43-60.

Cruz, L.J. at al. (1976). *Verliger* **18**:302-308.

Cruz, L.J. et al. (1987). *J. Biol. Chem.* **262**:15821-15824.

Ettinger, L.J. et al. (1978). *Cancer* **41**:1270-1273.

Fainzilber, M. et al. (1998). *Biochemistry* **37**:1470-1477.

Goodman and Gilman's The Pharmacological Basis of Therapeutics, Seventh Ed., Gilman, A.G. et al., eds., Macmillan Publishing Co., New York (1985).

Hammerland et al. (1992). *Eur. J. Pharmacol.* **226**:239-244.

Heading, C. (1999). *Curr. Opin. CPNS Invest. Drugs* **1**:153-166.

Hopkins, C. et al. (1995). *J. Biol. Chem.* **270**:22361-22367.

Horiki, K. et al. (1978). *Chemistry Letters* 165-68.

Hubry, V. et al. (1994). *Reactive Polymers* **22**:231-241.

Hylden, J.L.K.and Wilcox, G. (1980). *Eur. J. Pharmacol.* **67**:313-316.

Jacobsen, R. et al. (1997). *J. Biol. Chem.* **272**:22531-22537.

Jimenez, E.C. et al. (1996). *J. Biol. Chem.* **271**:28002-28005.

Kaiser et al. (1970). *Anal. Biochem.* **34**:595.

Kapoor (1970). *J. Pharm. Sci.* **59**:1-27.

Kornreich, W.D. et al. (1986). U.S. Patent No. 4,569,967.

Kruszynski, M. et al. (1990). *Experientia* **46**:771-773.

Luer, M.S. & Hatton, J. (1993). *Annals Pharmcotherapy* **27**:912-921.

Liu, H. et al. (1997). *Nature* **386**:721-724.

Malmberg, A.B. and Basbaum, A.I. (1998). *Pain* **76**:215-222.

Maric, M. et al. (1989). *Physiol. Pharmacol.* **67**:1437-1441.

Martinez, J.S. et al. (1995). *Biochem.* **34**:14519-14526.

Mayer, E.A. et al. (1994). *Gastroenterology* **107**:271-293.

McIntosh, J. M. et al. (1998). *Methods Enzymol.* **294**:605-624.

The Merck Manual of Diagnosis and Therapy, 16 Ed., Berkow, R. et al., eds., Merck Research Laboratories, Rahway, N.J., pp. 1436-1445 (1992).

Methoden der Organischen Chemie (Houben-Weyl): Synthese von Peptiden, E. Wunsch (Ed.), Georg Thieme Verlag, Stuttgart, Ger. (1974).

Nehlig, A. et al. (1990). Effects of phenobarbital in the developing rat brain. In *Neonatal Seizures*, Wasterlain, C.G. and Vertt, P. (eds.), Raven Press, New York, pp. 285-194.

Nishiuchi, Y. et al. (1993). *Int. J. Pept. Protein Res.* **42**:533-538.

Olivera, B.M. et al. (1984). U.S. Patent 4,447,356.

Olivera, B.M. et al. (1985). *Science* **230**:1338-1343.

Olivera, B.M. et al. (1990). *Science* **249**:257-263.

Olivera, B.M. et al. (1996). U.S. Patent 5,514,774.

Ornstein, et al. (1993). *Biorganic Medicinal Chemistry Letters* **3**:43-48.

Remington's Pharmaceutical Sciences, 18th Ed. (1990, Mack Publishing Co., Easton, PA).

Rivier, J.R. et al. (1978). *Biopolymers* **17**:1927-38.

Rivier, J.R. et al. (1987). *Biochem.* **26**:8508-8512.

Sambrook, J. et al. (1989). *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

Shon, K.-J. et al. (1994). *Biochemistry* **33**:11420-11425.

Shon, K.-J. et al. (1997). *Biochemistry* **36**:9581-9587.

Stewart and Young, *Solid-Phase Peptide Synthesis*, Freeman & Co., San Francisco, CA (1969).

Vale et al. (1978). U.S. Patent 4,105,603.

Troupin, A.S. et al. (1986). MK-801. In *New Anticonvulsant Drugs, Current Problems in Epilepsy 4*, Meldrum, B.S. and Porter, R.J. (eds.), John Libbey, London, pp. 191-202.

Van de Steen, P. et al. (1998). *Critical Rev. in Biochem. and Mol. Biol.* **33**:151-208.

White, H.S., et al. (1992). *Epilepsy Res.* **12**:217-226.

White, H.S., et al. (1995). Experimental Selection, Quantification, and Evaluation of Antiepileptic Drugs. In *Antiepileptic Drugs*, 4th Ed., Levy, R.H., eds., Raven Press, N.Y., pp. 99-110.

Wong, E.H.P. et al. (1986). *Proc. Natl. Acad. Sci. USA* **83**:7104-7108.

Zhou L.M., et al. (1996). *J. Neurochem.* **66**:620-628.

Zimm, S. et al. (1984). *Cancer Res.* **44**:1698-1701.

U.S. Patent No. 3,842,067.

U.S. Patent No. 3,862,925.

U.S. Patent No. 3,972,859.

U.S. Patent No. 5,514,774.

U.S. Patent No. 5,550,050.

U.S. Patent No. 5,670,622.

U.S. Patent No. 5,719,264.

U.S. Patent No. 5,844,077.

U.S. Patent No. 5,889,147.

U.S. Patent No. 5,969,096.

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